

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:16:05 : Search time 10 Seconds
(without alignments)
38.720 Million cell updates/sec

Title: US-09-613-355D-3
Perfect score: 10
Sequence: 1 NLGEHPVCD5 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6	60.0	373	1 YIA6_YEAST	P40556 saccharomyc
2	6	60.0	708	1 RAFA_ECOLI	P16551 escherichia
3	6	60.0	808	1 GC51_SCHPO	O14255 schizosacch
4	6	60.0	898	1 T021_SYNY3	P73810 synecocyst
5	5	50.0	31	1 DEF2_MESAU	P81466 mesocricetu
6	5	50.0	33	1 DEF4_MESAU	P03240 human adeno
7	5	50.0	114	1 E413_ADE02	P21377 naja atra
8	5	50.0	116	1 NGF_NAJAT	P01140 naja naja
9	5	50.0	116	1 NGF_NAJNA	P15743 gallus gall
10	5	50.0	119	1 PTHV_CHICK	P47038 saccharomyc
11	5	50.0	131	1 YJG4_YEAST	P07376 salmonella
12	5	50.0	146	1 MUCA_SALTY	O29055 archaeoglob
13	5	50.0	149	1 YC13_ARCFU	O12933 orgyia pseu
14	5	50.0	152	1 S0DC_NPVOP	P29340 saccharomyc
15	5	50.0	183	1 UBCC_YEAST	P22237 dictyosteli
16	5	50.0	209	1 NUGM_DICDI	O53698 mycobacteri
17	5	50.0	261	1 TAM_MYCTU	P14295 lactobacilli
18	5	50.0	309	1 DHL2_LACCO	P72065 mycobacteri
19	5	50.0	347	1 GYRA_MVLXE	P40013 saccharomyc
20	5	50.0	427	1 BIMI_YEAST	P23202 saccharomyc
21	5	50.0	354	1 URE2_YEAST	O40531 nicotiana t
22	5	50.0	371	1 NTF6_TOBAC	G92398 schizosacch
23	5	50.0	422	1 SPML_SCHPO	P12539 mouse adeno
24	5	50.0	449	1 PIV2_ADEM1	O03522 bacillus su
25	5	50.0	451	1 MURD_BACSU	P34809 cryptococcu
26	5	50.0	491	1 NMT_CRYNE	P37118 solanum mel
27	5	50.0	505	1 C712_SOLME	P37117 solanum mel
28	5	50.0	507	1 C714_SOLME	O64437 oryza sativ
29	5	50.0	510	1 INOI_ORYSA	P25918 mus musculu
30	5	50.0	547	1 CD19_MOUSE	P78753 schizosacch
31	5	50.0	556	1 ASNS_SCHPO	O14013 schizosacch
32	5	50.0	556	1 YDPA_SCHPO	P23731 ascaris suu
33	5	50.0	589	1 IFEB_ASCSU	

34	5	50.0	613	1 ISPG_CHEPN	Q928h0 chlamydia p
35	5	50.0	676	1 QRL_COTJA	P23499 coturnix co
36	5	50.0	679	1 DNLJ_HAEIN	P43813 haemophilus
37	5	50.0	731	1 DNLJ_ZYMMO	P24719 zymomonas m
38	5	50.0	738	1 ECT2_MOUSE	Q07139 mus musculu
39	5	50.0	741	1 RN5A_HUMAN	Q05823 homo sapien
40	5	50.0	768	1 PARC_NEIGO	P48374 neisseria g
41	5	50.0	776	1 SM4F_RAT	Q92143 rattus norv
42	5	50.0	777	1 SM4F_MOUSE	Q92143 mus musculu
43	5	50.0	813	1 VGLH_HSVMD	P36336 marek's dis
44	5	50.0	839	1 TOP1_SYNE7	P34185 synecococc
45	5	50.0	883	1 ECT2_HUMAN	Q9H8v3 homo sapien

ALIGNMENTS

RESULT 1
YIA6_YEAST STANDARD; PRT: 373 AA.
AC P40556;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Putative mitochondrial carrier YIL006W.
GN YIL006W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N A
RC STRAIN=5288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lyle G., Moule S., Moule N., Odell C., Pearson D.,
RA Rajadream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC entities requires a license agreement (see <http://www.ebi.ac.uk/submit/submit.html> or send an email to license@ebi-sib.ch).
CC -----
CC EMBL: Z38113; CAAB6245.1;
CC PIR: S48451; S48451.
CC SGD: S0001268; YIL006W.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carrier_3.
CC PROSITE: PS00215; MITOCH_CARRIER; 2.
CC Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
CC Transmembrane; Transport.
CC TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
SQ SEQUENCE 373 AA; 41954 MW; 976C767C1D40E8DF CRC64;
Query Match 60.0%; Score 6; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEHP 6
|||||

RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
 CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
 CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
 CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
 CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
 CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
 CC -!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
 CC FAMILY.
 CC
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 CC
 CC -----
 CC EMBL: D90909; BAA17864.1; -;
 CC HSSP: P06612; LECL.
 CC InterPro: IPR003601; DNATopI_ATP_bind.
 CC InterPro: IPR003602; DNATopI_DNA_bind.
 CC InterPro: IPR000380; Pro.topoisomerase.
 CC InterPro: IPR002936; Toprim.
 CC Pfam: PF01131; Topoisom_bac; 1.
 CC Pfam: PF01751; Toprim; 1.
 CC PRINTS: PR00417; PRTPISMRASEI.
 CC SMART: SM00437; TOPIAC; 1.
 CC SMART: SM00436; TOPIRC; 1.
 CC SMART: SM00493; TOPIRM; 1.
 CC PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA-binding; Complete proteome.
 FT ACT_SITE 320 320
 FT ACT_SITE 320 320
 SQ SEQUENCE 898 AA; 99340 MW; 941666597398EB3 CRC64;

 Query Match 60.0%; Score 6; DB 1; Length 898;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

 QY 1 NLGHP 6
 DB 721 NLGHP 726

 RESULT 5
 DEF2_MESAU STANDARD: PRT: 31 AA.
 AC P81466;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Neutrophil defensin 2 (HAMP-2).
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97045125; PubMed=8890190;
 RA Mak P., Wojcik K., Thøgersen I.B., Dubin A.;
 RT "Isolation, antimicrobial activities, and primary structures of
 RT hamster neutrophil defensins.";
 RL Infect. Immun. 64:4444-4449(1996).
 CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE
 CC BACTERIA. LOW ANTI-FUNGI ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN
 CC PEPTIDES.
 CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL
 CC AMINO ACID REMOVAL FROM HAMP-4.
 CC InterPro: IPR001271; Defensin.
 CC Pfam: PF00323; defensins; 1.
 CC SMART: SM00048; DEFSN; 1.
 CC PROSITE: PS00269; DEFENSIN; 1.
 CC Defensin; Antibiotic; Fungicide.
 KW DISULFID 3 31 BY SIMILARITY.
 FT DISULFID 5 20 BY SIMILARITY.
 FT DISULFID 10 30 BY SIMILARITY.
 SQ SEQUENCE 33 AA; 3821 MW; 23097FE7D474AD65 CRC64;

 Query Match 50.0%; Score 5; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

 QY 6 PVCD5 10
 DB 8 PVCD5 12

 RESULT 7
 E413_ADE02

RL Infect. Immun. 64:4444-4449(1996).
 CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE
 CC BACTERIA. LOW ANTI-FUNGI ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN
 CC PEPTIDES.
 CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL
 CC AMINO ACID REMOVAL FROM HAMP-4.
 CC InterPro: IPR001271; Defensin.
 CC Pfam: PF00323; defensins; 1.
 CC SMART: SM00048; DEFSN; 1.
 CC PROSITE: PS00269; DEFENSIN; 1.
 CC Defensin; Antibiotic; Fungicide.
 KW DISULFID 1 29 BY SIMILARITY.
 FT DISULFID 3 18 BY SIMILARITY.
 FT DISULFID 8 28 BY SIMILARITY.
 SQ SEQUENCE 31 AA; 3621 MW; 3DE9E747D474AD34 CRC64;

 Query Match 50.0%; Score 5; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

 QY 6 PVCD5 10
 DB 6 PVCD5 10

RESULT 6
 DEF4_MESAU STANDARD: PRT: 33 AA.
 ID DEF4_MESAU
 AC P81468;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Neutrophil defensin 4 (HAMP-4).
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97045125; PubMed=8890190;
 RA Mak P., Wojcik K., Thøgersen I.B., Dubin A.;
 RT "Isolation, antimicrobial activities, and primary structures of
 RT hamster neutrophil defensins.";
 RL Infect. Immun. 64:4444-4449(1996).
 CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE
 CC BACTERIA. LOW ANTI-FUNGI ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN
 CC PEPTIDES.
 CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL
 CC AMINO ACID REMOVAL FROM HAMP-4.
 CC InterPro: IPR001271; Defensin.
 CC Pfam: PF00323; defensins; 1.
 CC SMART: SM00048; DEFSN; 1.
 CC PROSITE: PS00269; DEFENSIN; 1.
 CC Defensin; Antibiotic; Fungicide.
 KW DISULFID 3 31 BY SIMILARITY.
 FT DISULFID 5 20 BY SIMILARITY.
 FT DISULFID 10 30 BY SIMILARITY.
 SQ SEQUENCE 33 AA; 3821 MW; 23097FE7D474AD65 CRC64;

 Query Match 50.0%; Score 5; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

 QY 6 PVCD5 10
 DB 8 PVCD5 12

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ID E413_ADE02 STANDARD: PRT: 114 AA.
 AC P03240;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Probable early E4 13 kDa protein.
 OS Human adenovirus type 2.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82059444; PubMed=6985482;
 RA Herisse J., Rigolet M., Dupont de Dinechin S., Calibert F.;
 RT "Nucleotide sequence of adenovirus 2 DNA fragment encoding for the
 RT carboxylic region of the fiber protein and the entire E4 region.";
 RL Nucleic Acids Res. 9:4021-4042(1981).
 CC -! MISCELLANEOUS; THIS PROBABLE PROTEIN WAS ASSIGNED BY CORRELATING
 CC EM DATA AND S1 DIGESTION STUDIES.
 CC -----
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 CC -----
 CC EMBL: J01917; -; NOT_ANNOTATED_CDS.
 DR PIR: A03806; Q4ADD2.
 KW Early protein.
 SQ SEQUENCE 114 AA, 13121 MW; 72FB72749D563457 CRC64;

 Query Match 50.0%; Score 5; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 PVCD5 10
 DB 10 PVCD5 14

 RESULT 8
 NGF_NAJAT STANDARD: PRT: 116 AA.
 ID NGF_NAJAT
 AC P21377;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Nerve growth factor (NGF).
 OS Naja atra (Chinese cobra), and
 OS Naja naja kaouthia (Monocled cobra) (Naja naja siamensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=8656, 8649;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.n.atra; TISSUE=Venom;
 RX MEDLINE=90147847; PubMed=2619756;
 RA Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;
 RT "Amino acid sequence of nerve growth factor purified from the venom
 RT of the Formosan cobra Naja naja atra.";
 RL Biochem. Int. 19:909-917(1989).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=N.n.kaouthia; TISSUE=Venom;
 RX MEDLINE=91138755; PubMed=1995338;
 PA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
 RT "Amino acid sequences of nerve growth factors derived from cobra
 RT venoms.";
 RL FEBS Lett. 279:38-40(1991).
 CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT

CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC PIR: S13965; S13965.
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF_1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRODOM: PD002052; NGF_1.
 DR SMART: SM00140; NGF_1.
 DR PROSITE: PS00248; NGF_1; 1.
 DP PROSITE: PS0270; NGF_2; 1.
 KW Growth factor
 FT DISULFID 14 78 BY SIMILARITY.
 FT DISULFID 56 106 BY SIMILARITY.
 FT DISULFID 66 108 BY SIMILARITY.
 FT SEQUENCE 116 AA; 13064 MW; DAB35421093F3B06 CRC64;
 SQ
 Query Match 50.0%; Score 5; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 NLGEH 5
 DB 7 NLGEH 11

 RESULT 9
 NGF_NAJNA STANDARD: PRT: 116 AA.
 ID NGF_NAJNA
 AC P01140;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Nerve growth factor (NGF).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=91138755; PubMed=1995338;
 RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
 RT "Amino acid sequences of nerve growth factors derived from cobra
 RT venoms.";
 RL FEBS Lett. 279:38-40(1991).
 RN [2]
 RP PRELIMINARY SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=76114772; PubMed=1247508;
 RA Hoque-Angeletti R.A., Frazier W.A., Jacobs J.W., Niall H.D.,
 RA Bradshaw R.A.;
 RT "Purification, characterization, and partial amino acid sequence of
 RT nerve growth factor from cobra venom.";
 RL Biochemistry 15:26-34(1976).
 CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC PIR: A01401; NGNXXI.
 DR PIR: S13927; S13927.
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR002072; NGF.

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DR Pfam: PF00243; NGF; 1
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
KW Growth factor.
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
SQ SEQUENCE 116 AA; 13022 MW; DAB346B1093E7E06 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
DB 7 NLGEH 11

RESULT 10
PTHY_CHICK
ID PTHY_CHICK STANDARD; PRT; 119 AA.
AC P15743;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (PTH).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=89219100; PubMed=2710135;
RA Russell J., Sherwood L.M.;
RT "Nucleotide sequence of the DNA complementary to avian (chicken)
RT preproparathyroid hormone mRNA and the deduced sequence of the
RT hormone precursor."
RL Mol. Endocrinol. 3:325-331(1989).
[2]

SEQUENCE FROM N.A.
RP MEDLINE=89284968; PubMed=3251402;
RX Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA Kronenberg H.M.;
RT "Nucleotide sequence of cloned cDNAs encoding chicken
RT preproparathyroid hormone."
FL J. Bone Miner. Res. 3:689-698(1988).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY INCREASING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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EMBL; M31604; AAA49093.1; -
DR EMBL; M36522; AAB02866.1; -
DR PIR; A34937; A34937.
DR HSP; P01270; LHPV.
DR InterPro: IPR001415; Parathyroid.
DR InterPro: IPR003625; Parathyroid_hormn_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Parathyroid_hormn_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.

KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 112 PARATHYROID HORMONE.
SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6F CRC64;

Query Match 50.0%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
DB 41 NLGEH 45

RESULT 11
YJG4_YEAST
ID YJG4_YEAST STANDARD; PRT; 131 AA.
AC P47038; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 13.9 kDa protein in SMC3-MRPL8 intergenic region.
GN YJL064W OR J1120 OR HRC131.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of
RT Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
RT 18."
RL Yeast 11:57-60(1995).

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; Z49340; CAA89356.1; -
DR EMBL; Z34288; CAA84058.1; -
DR SGD; S0003600; YJL064W.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 13854 MW; 736E72054593EF3 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
DB 109 NLGEH 113

RESULT 12
MUC4_SALTY
ID MUC4_SALTY STANDARD; PRT; 146 AA.
AC P07376; P14302;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Muc4 protein (EC 3.4.21.-) [Contains: Muc4 protein].
DE MUC4.
OS Salmonella typhimurium, and
OS Escherichia coli.
OC Plasmid IncN PKM101, and Plasmid IncN R46.

```


Wed Oct 23 14:06:09 2002

 CC -1- SIMILARITY: BELONGS TO THE CU,ZN SUPEROXIDE DISMUTASE FAMILY.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X65479; CAA46467.1; -
 CC EMBL: Z72918; CAA97146.1; -
 CC PIR: S29088; S29088
 CC HSSP: P15731; LQCO
 CC SGD: S0003365; PEX4
 CC InterPro: IPR000608; UBQ_conjugat.
 CC Pfam: PF00179; UO_con: 1
 CC SMART: SM00212; UBQC; 1
 CC PROSITE: PS00183; UBIQUITIN_CONJUGAT_1; 1
 CC PROSITE: PS0127; UBIQUITIN_CONJUGAT_2; 1
 CC UBIQUITIN conjugation; Ligase; Multigene family; Peroxisome.
 KW BINDING 115 115 UBIQUITIN (BY SIMILARITY).
 FT SEQUENCE 183 AA; 21118 MW; D4E438B689F76CAD CRC64;
 SQ
 Query Match 50.0%; Score 5; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PNCDS 10
 Db 144 PNCDS 148
 Search completed: October 23, 2002, 13:19:52
 Job time : 11 secs

 CC -1- SIMILARITY: BELONGS TO THE CU,ZN SUPEROXIDE DISMUTASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U75930; AAC59028.1; -
 CC HSSP: P00441; 4SOD
 CC InterPro: IPR001424; SOD_CU_ZN
 CC Pfam: PF00080; sdcu; 1
 CC PRINTS: PR00068; CUZNDISMUTASE
 CC PRODOM: PD000469; SOD_CU_ZN; 1
 CC PROSITE: PS00087; SOD_CU_ZN_1; 1
 CC PROSITE: PS00332; SOD_CU_ZN_2; 1
 CC Late protein; Oxidoreductase; Copper; Zinc.
 KW METAL 43 43 COPPER (BY SIMILARITY).
 FT METAL 45 45 COPPER (BY SIMILARITY).
 FT METAL 60 60 COPPER AND ZINC (BY SIMILARITY).
 FT METAL 68 68 ZINC (BY SIMILARITY).
 FT METAL 77 77 ZINC (BY SIMILARITY).
 FT METAL 80 80 ZINC (BY SIMILARITY).
 FT METAL 118 118 COPPER (BY SIMILARITY).
 FT DISULFID 54 144 BY SIMILARITY.
 SQ SEQUENCE 152 AA; 15855 MW; 2B78743FFB47BB0 CRC64;
 Query Match 50.0%; Score 5; DB 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LGHPH 6
 Db 126 LGHPH 130
 RESULT 15
 UBCX_YEAST STANDARD; PRT; 183 AA.
 AC P29340;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Ubiquitin-conjugating enzyme E2-21 kDa (EC 6.3.2.19)
 DE (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (Peroxin-4).
 GN PEX4 OR PAS2 OR UBC10 OR YGR133W. yeast.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92396219; PubMed=1326082;
 RA Wiebel F.F., Kunau W.-H.;
 RT "The Pas2 protein essential for peroxisome biogenesis is related to
 RT ubiquitin-conjugating enzymes.";
 RL Nature 359:73-76(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talia E.,
 RA Nawrocki A., del Bino S., Goffeau A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO
 CC OTHER PROTEINS. ESSENTIAL FOR PEROXISOME BIOGENESIS.
 CC -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 CC diphosphate + protein N-ubiquityllysine.
 CC -1- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
 CC -1- SUBCELLULAR LOCATION: Peroxisomal.
 CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR
 CC UBIQUITIN-THIOLESTER FORMATION.
 CC -1- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

us-09-613-355d-3.ra1

Wed Oct 23 14:06:04 2002

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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:14:14 Search time 13 Seconds
(without alignments)
18,789 Million cell updates/sec

Title: US-09-613-355D-3
Perfect score: 10
Sequence: 1 NLGHPVCDs 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	50.0	35	2	US-08-142-551B-51
2	5	50.0	120	4	US-09-660-552-31
3	5	50.0	146	4	US-09-660-552-29
4	5	50.0	344	1	US-08-446-919A-4
5	5	50.0	371	2	US-08-837-593-8
6	5	50.0	600	3	US-08-904-871-3
7	5	50.0	607	3	US-09-335-409-9
8	5	50.0	607	4	US-09-568-102-9
9	5	50.0	607	4	US-09-567-969-9
10	5	50.0	607	4	US-09-568-480-9
11	5	50.0	607	4	US-09-568-486-9
12	5	50.0	607	4	US-09-568-472-9
13	5	50.0	741	2	US-08-462-481-2
14	5	50.0	741	2	US-08-436-771-2
15	5	50.0	741	2	US-08-436-771-4
16	5	50.0	741	2	US-08-434-998-2
17	5	50.0	741	2	US-08-434-998-4
18	5	50.0	741	2	US-08-487-797-2
19	5	50.0	741	2	US-08-487-797-4
20	5	50.0	741	2	US-08-701-005A-2
21	5	50.0	741	2	US-08-479-895-2
22	5	50.0	741	3	US-08-943-956A-2
23	5	50.0	741	5	PCT-US95-02058-2
24	5	50.0	741	5	PCT-US95-02058-4
25	5	50.0	2273	4	US-09-426-998-5
26	4	40.0	5	3	US-08-802-981-209
27	4	40.0	7	3	US-08-802-981-207

Sequence 14, Appl
Sequence 11, Appl
Sequence 204, Appl
Sequence 11, Appl
Sequence 11, Appl
Patent No. 5190919
Patent No. 5190919
Patent No. 5190919
Sequence 22, Appl
Patent No. 5190919
Sequence 23, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 1, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 50, Appl
Sequence 8, Appl

1 US-08-201-046A-14
2 US-08-726-136-11
3 US-08-802-981-204
4 US-09-103-434-11
5 US-09-687-594-11
6 5190919-38
7 5190919-40
8 5190919-7
9 5190919-31
10 5190919-22
11 US-08-201-046A-23
12 US-08-036-555B-8
13 US-08-469-569-8
14 US-08-218-023-1
15 US-08-249-322A-8
16 US-08-469-526A-8
17 US-08-480-190-50
18 US-08-734-591A-8

ALIGNMENTS

RESULT 1
US-08-142-551B-51
Sequence 51, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND RECOMBINANT DNA VECTORS ENCODING SAME
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site

us-09-613-355d-3.ra1

Wed Oct 23 14:06:04 2002

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; LOCATION: 35
; OTHER INFORMATION: /note= "where "xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-51
Query Match 50.0%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEH 5
DB 10 NLGEH 14
RESULT 2
US-09-660-552-31
; Sequence 31, Application US/09660552
; Patent No. 633178
; GENERAL INFORMATION:
; APPLICANT: LIVNEH, Zvi
; APPLICANT: BACHER REUVEN, Nina
; APPLICANT: TOMER, Guy
; TITLE OF INVENTION: METHODS OF REPLICATING A DNA MOLECULE FOR REPAIR OF DNA
; TITLE OF INVENTION: LESION DAMAGE
; TITLE OF INVENTION: OR FOR MUTAGENESIS
; FILE REFERENCE: LIVNEH-1B
; CURRENT FILING DATE: 2000-09-12
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/627,399
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 69/145,162
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant MuA'
US-09-660-552-31
Query Match 50.0%; Score 5; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EHPVC 8
DB 114 EHPVC 118
RESULT 3
US-09-660-552-29
; Sequence 29, Application US/09660552
; Patent No. 633178
; GENERAL INFORMATION:
; APPLICANT: LIVNEH, Zvi
; APPLICANT: BACHER REUVEN, Nina
; APPLICANT: TOMER, Guy
; TITLE OF INVENTION: METHODS OF REPLICATING A DNA MOLECULE FOR REPAIR OF DNA
; TITLE OF INVENTION: LESION DAMAGE
; FILE REFERENCE: LIVNEH-1B
; CURRENT FILING DATE: 2000-09-12
; PRIOR FILING DATE: 09/627,399
; PRIOR APPLICATION NUMBER: 60/146,162
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Conjugative plasmid
US-09-660-552-29
Query Match 50.0%; Score 5; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EHPVC 8
DB 140 EHPVC 144
RESULT 4
US-08-446-919A-4
; Sequence 4, Application US/08446919A
; Patent No. 5736389
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: EB1 Gene Product Binds to APC
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hanner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,919A
; FILING DATE:
; CLASSIFICATION: 544
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagar, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.49255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; IMMEDIATE SOURCE:
; CLONE: Yeo016p
US-08-446-919A-4
Query Match 50.0%; Score 5; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEH 5
DB 292 NLGEH 246
RESULT 5
US-08-837-593-8
; Sequence 8, Application US/08837593
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Wed Oct 23 14:06:04 2002

; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuguo
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-8

Query Match 50.0%; Score 5; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10
DB 334 PVCDS 338

RESULT 6
US-08-904-871-3
; Sequence 3, Application US/08904871
; Patent No. 6046014
; GENERAL INFORMATION:
; APPLICANT: Lagarias, John C
; APPLICANT: Murphy, John T
; TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
; FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
; CURRENT APPLICATION NUMBER: US/08/904,871
; CURRENT FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,217
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:: Sequence
; OTHER INFORMATION: alignment Fig. 6 Alphy
; US-08-904-871-3

Query Match 50.0%; Score 5; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7
DB 118 GEHPV 122

RESULT 7
US-09-335-409-9
; Sequence 9, Application US/09335409
; Patent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILOXONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-335-409-9

Query Match 50.0%; Score 5; DB 3; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 487 LGEHP 491

RESULT 8
US-09-568-102-9
; Sequence 9, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILOXONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,102
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-102-9

us-09-613-355d-3.ra1

wed Oct 23 14:06:04 2002

Query Match 50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
|
|
|
|
|
Db 487 LGEHP 491

RESULT 9
US-09-567-969-9
; Sequence 9, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-9

Query Match 50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
|
|
|
|
|
Db 487 LGEHP 491

RESULT 10
US-09-568-480-9
; Sequence 9, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-480-9

Query Match 50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
|
|
|
|
|
Db 487 LGEHP 491

RESULT 11
US-09-568-486-9
; Sequence 9, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-486-9

Query Match 50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
|
|
|
|
|
Db 487 LGEHP 491

RESULT 12
US-09-568-472-9
; Sequence 9, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-9

Query Match 50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
|
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|
|
|
Db 487 LGEHP 491

```

RESULT 13
US-08-462-481-2
; Sequence 2, Application US/08462481
; Patent No. 5840577
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Alvin
; TITLE OF INVENTION: Aulmal 2'-5A' Dependent RNases and
; TITLE OF INVENTION: Encoding Sequence Therefor
; Patent No. 5840577
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.481
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028.086
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-481-2

Query Match 50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 668 NLGEH 672

RESULT 14
US-08-436-771-2
; Sequence 2, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498

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; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-771-2

Query Match 50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 668 NLGEH 672

RESULT 15
US-08-436-771-4
; Sequence 4, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498

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us-09-613-355d-3.ra1

Wed Oct 23 14:06:04 2002

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: TELEFAX: 305/764/4996
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 741 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
US-08-436-771-4
Query Match      50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 668 NLGEH 672

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Search completed: October 23, 2002, 12:16:18
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:18:20 : Search time 16. Seconds
(without alignments)
60.056 Million cell updates/sec

Title: US-09-613-355D-3
Perfect score: 10
Sequence: 1 NLGHPVCD5 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR71.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	60.0	373	2 S48451	probable membrane
2	6	60.0	414	2 E75636	hypothetical prote
3	6	60.0	708	1 A43717	alpha-galactosidas
4	6	60.0	808	2 T39059	probable mannosyl-
5	6	60.0	898	2 S74903	DNA topoisomerase
6	6	60.0	925	2 T16235	hypothetical prote
7	5	50.0	90	2 S12848	maturatin (piva2)
8	5	50.0	114	1 Q4ADD2	early E4 13K prote
9	5	50.0	116	1 NGJX1	nerve growth facto
10	5	50.0	116	2 A58566	nerve growth facto
11	5	50.0	116	2 C72549	hypothetical prote
12	5	50.0	119	2 A34937	parathyroid hormon
13	5	50.0	131	2 S50807	probable membrane
14	5	50.0	143	2 B84459	hypothetical prote
15	5	50.0	145	1 ZWECAP	mucA protein - Esc
16	5	50.0	146	2 S06775	muca protein - Sal
17	5	50.0	149	2 D69401	hypothetical prote
18	5	50.0	152	2 T10298	superoxide dismuta
19	5	50.0	154	2 PQ0465	beta C protein - p
20	5	50.0	168	2 S64830	hypothetical prote
21	5	50.0	172	2 B84008	hypothetical prote
22	5	50.0	179	2 S29088	ubiquitin--protein
23	5	50.0	183	2 D87567	conserved hypothet
24	5	50.0	203	2 S25617	hypothetical prote
25	5	50.0	209	2 S12247	NADH dehydrogenase
26	5	50.0	209	2 C84162	hypothetical prote
27	5	50.0	211	2 S48779	LI protein - human
28	5	50.0	224	2 T51072	hypothetical prote
29	5	50.0	238	2 T51072	hypothetical prote

30	5	50.0	239	2 F83366	conserved hypothet
31	5	50.0	242	2 C83631	probable carbonic
32	5	50.0	246	2 A59218	nerve growth facto
33	5	50.0	261	2 D70837	hypothetical prote
34	5	50.0	274	2 T32736	hypothetical prote
35	5	50.0	284	2 T36286	pyrroline-5-carbox
36	5	50.0	288	2 B84862	hypothetical prote
37	5	50.0	291	2 AF3264	4-hydroxybutyryl-C
38	5	50.0	297	2 T46414	hypothetical prote
39	5	50.0	301	2 A32814	flagellar filament
40	5	50.0	310	2 JQ0114	L-2-hydroxyisocapr
41	5	50.0	322	2 T32263	hypothetical prote
42	5	50.0	344	2 S50474	polymetase - Berne
43	5	50.0	351	2 S11237	glutathione transf
44	5	50.0	354	2 A39609	hypothetical prote
45	5	50.0	355	2 C70194	hypothetical prote

ALIGNMENTS

RESULT 1
S48451
probable membrane protein Y1006w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 31-Mar-2000
C:Accession: S48451
R:Rowley, N.
submitted to the EMBL Data Library, August 1994
A:Reference number: S48442
A:Accession: S48451
A:Molecule type: DNA
A:Residues: 1-373 <ROW>
A:Cross-references: GB:Z47047; EMBL:Z38113; NID:9603997; PID:9763340; MIPS:Y1006w
C:Genetics:
A:Map position: 9L
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:74-167/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:79-95/Domain: transmembrane #status predicted <TM1>
F:173-264/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:236-252/Domain: transmembrane #status predicted <TM2>
F:275-365/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 60.0%; Score 6; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6
|||
DB 209 NLGHP 214

RESULT 2
E75636
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75636
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75636
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <WHI>
A:Cross-references: GB:AE001827; NID:96460959; PID:96460981; TIGR:DR000000000

A:Experimental source: strain R1
C:Genetics:
A:Gene: DR00015

A:Map position: plasmid
A:Genome: plasmid
A:Note: plasmid Cpl

Query Match 60.0%; Score 6; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7
| | | | |
Db 301 LGEHPV 306

RESULT 3

A43717 alpha-galactosidase (EC 3.2.1.22), raffinose-specific - Escherichia coli plasmid D1021

C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A43717, B35160

R:Aslanidis, C.; Schmid, K.; Schmitt, P.

J. Bacteriol. 171, 6753-6763, 1989

A:Title: Nucleotide sequences and operon structure of plasmid-borne genes mediating uptake of galactose

A:Reference number: A43717; MUID:90078124

A:Accession: A43717

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-708 <ASL>

A:Cross-references: GB:M27273; NID:g147504; PIDN:AAA24497.1; PID:g147505

R:Aslanidis, C.; Schmitt, R.

J. Bacteriol. 172, 2178-2180, 1990

A:Title: Regulatory elements of the raffinose operon: nucleotide sequences of operator and promoter

A:Reference number: A35160; MUID:90202743

A:Accession: B35160

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <AS2>

A:Cross-references: GB:M29849; NID:g147508; PIDN:AAA24501.1; PID:g551828

C:Genetics:

A:Gene: rafa

A:Genome: plasmid

A:Complex: homotetramer

C:Function:

A:Description: catalyzes the hydrolysis of raffinose to galactose and sucrose

C:Superfamily: raffinose-specific alpha-galactosidase

C:Keywords: glycoprotein; glycosidase; hydrolase

QY 2 LGEHPV 7

| | | | |

Db 430 LGEHPV 435

RESULT 4

T39059 probable mannose-oligosaccharide glucosidase (EC 3.2.1.106) - fission yeast (Schizosaccharomyces octosporus)

C:Species: Schizosaccharomyces octosporus

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000

R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: 221824

A:Accession: T39059

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-808 <OLI>

A:Cross-references: EMBL:298603; PIDN:CAP11295.1; GSPDB:GN00066; SPDB:SPAC6G10.09

A:Experimental source: strain 972h-; cosmid c6G10

C:Genetics:

A:Gene: SPDB:SPAC6G10.09

A:Map position: 1

A:Introns: 80/1
C:Keywords: glycosidase; hydrolase

Query Match 60.0%; Score 6; DB 2; Length 808;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7
| | | | |
Db 192 LGEHPV 197

RESULT 5

S74903 DNA topoisomerase I - *Synechocystis* sp. (strain PCC 6803)

N:Alternate names: protein sir2058

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S74903

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, J.

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S74903

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-898 <KAN>

A:Cross-references: EMBL:U09009; GB:AB201339; NID:g1652844; PIDN:PA17864.1; PID:g165

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: topA

C:Superfamily: bacterial type I DNA topoisomerase

Query Match 60.0%; Score 6; DB 2; Length 898;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEHP 6

| | | | |

Db 721 NLGEHP 726

RESULT 6

T16235

hypothetical protein F32A5.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16235

R:Pauley, A.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of *C. elegans* cosmid F32A5.

A:Reference number: Z18482

A:Accession: T16235

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-925 <PAU>

A:Cross-references: EMBL:U09864; NID:g069026; FID:g669027; PIDN:AA34556.1; GSP:F32A

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: GSP:F32A5.1

A:Introns: 36/3; 142/1, 172/2, 263/3; 340/1, 351/1 56/2, 56/3, 57/2, 57/3 812/1

Query Match 60.0%; Score 6; DB 2; Length 925;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8

| | | | |

Db 6 GEHPVC 11

RESULT 7

SI2848
maturation (p1va2) protein - mouse adenovirus 1 (fragment)
C:Species: Mastadenovirus mus1 (mouse adenovirus 1)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C:Accession: SI2848
R:King, S.C.; Spindler, K.R.
Nucleic Acids Res. 18, 4003, 1990
A:Title: Sequence of mouse adenovirus type 1 DNA encoding the amino terminus of protein
A:Reference number: SI2848; MUID:90326539
A:Accession: SI2848
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-90 <KRI>
C:Superfamily: adenovirus maturation protein

Query Match 50.0%; Score 5; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 18 NLGEH 22

RESULT 8

Q4ADD2
early E4 13K protein - human adenovirus 2
C:Species: Mastadenovirus h2 (human adenovirus 2)
A:Note: host Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 04-Mar-1994
C:Accession: A03806
R:Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.
Nucleic Acids Res. 9, 4023-4042, 1981
A:Title: Nucleotide sequence of adenovirus 2 DNA fragment encoding for the carboxylic re
A:Reference number: A93733; MUID:82059444
A:Accession: A03806
A:Molecule type: DNA
A:Residues: 1-114 <HER>
A:Note: this probable protein was assigned by correlating EM data and S1 digestion studi
C:Genetics:
A:Map position: 95.0-96.0
C:Superfamily: adenovirus early E4 13K protein
C:Keywords: early protein

Query Match 50.0%; Score 5; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVEDS 10
Db 10 PVEDS 14

RESULT 9

NGNJI
nerve growth factor - Indian cobra
C:Species: Naja naja naja (Indian cobra)
C:Date: 30-Nov-1980 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000
C:Accession: SI3927; A01401
R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.
FEBS Lett. 279, 38-40, 1991
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
A:Reference number: SI3927; MUID:91138755
A:Accession: SI3927
A:Molecule type: protein
A:Residues: 1-116 <INO>
A:Experimental source: venom
A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we hav
B:Hoque-Angeletti, R.A.; Frazier, W.A.; Jacobs, J.W.; Niall, H.D.; Bradshaw, R.A.
Biochemistry 15, 26-34, 1976
A:Title: Purification, characterization, and partial amino acid sequence of nerve growth

A:Reference number: A01401; MUID:76114772

A:Accession: A01401
A:Molecule type: protein
A:Residues: 1-11, p', 13-14, B', 16, TBT', 20-21, GV', 23-27, N', 29-31, AS', 34, S', 36-48,
15-116 <HOG>
A:Experimental source: venom
A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathet
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:14-78,56-106,66-108/Disulfide bonds: *status predicted

Query Match 50.0%; Score 5; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 7 NLGEH 11

RESULT 10

A58566
nerve growth factor - Chinese cobra
C:Species: Naja naja atra (Chinese cobra)
C:Date: 16-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: A58566
R:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.
Biochem. Int. 19, 909-917, 1989
A:Title: Amino acid sequence of nerve growth factor purified from the venom of the Fo
A:Reference number: A58566; MUID:90147847
A:Accession: A58566
A:Molecule type: protein
A:Residues: 1-116 <ODA>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathet
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:14-78,56-106,66-108/Disulfide bonds: *status predicted

Query Match 50.0%; Score 5; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 7 NLGEH 11

RESULT 11

C72549
hypothetical protein APE1679 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: C72549
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Grenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: C72549
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1116 <RAW>
A:Cross-references: DDBJ:AP0000062; NID:95105244, PID:RAA00000001; EMBL:U044466; FID:9

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1679

Query Match 50.0%; Score 5; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 47;

us-09-613-355d-3.rpr

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7
11111

Db 91 GEHPV 95

RESULT 12

parathyroid hormone precursor chicken
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: A34937; I50411
R:Russell, J.; Sherwood, L.M. 1989
Mol. Endocrinol. 3, 325-331.

A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone.
A:Reference number: A34937; MUID:89219100
A:Accession: A34937
A:Molecule type: mRNA
A:Residues: 1-119 <RUS>
A:Cross-references: GB:M31604; NID:q212767; PIDN:AAA49093.1; PID:q212768
R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-31/Domain: propeptide #status predicted <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-119/Product: parathyroid hormone #status predicted <MAT>

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-119 <RUS>
A:Cross-references: GB:M36522; NID:q212591; PIDN:AA802866.1; PID:q212592
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-31/Domain: propeptide #status predicted <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 50.0%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
11111

Db 41 NLGEH 45

RESULT 13

S50807
probable membrane protein YJL064w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein HKC131; hypothetical protein J1120
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C:Accession: S50807; S47126; S56838
R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A:Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A:Reference number: S50798; MUID:95282514
A:Accession: S50807
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-131 <VAN>
A:Cross-references: EMBL:Z34288; NID:g498992; PIDN:CAAB4058.1; PID:g499002
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A:Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A:Reference number: S47117
A:Accession: S47126
A:Molecule type: DNA
A:Residues: 1-131 <VAN>
A:Cross-references: EMBL:Z34288; NID:g498992; PID:g499002
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56835

A:Accession: S56838
A:Molecule type: DNA
A:Residues: 1-131 <POH>
A:Cross-references: EMBL:Z49340; NID:glu08212; PID:gi508214; MUID:YJL064w
C:Genetics:
A:Map position: 10L
A:Superfamily: Saccharomyces probable membrane protein YJL064w
C:Keywords: transmembrane protein

Query Match 50.0%; Score 5; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
11111

Db 109 NLGEH 113

RESULT 14

B84459
hypothetical protein At2g04580 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84459
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <STO>
A:Cross-references: GB:AE002093; NID:g4895106; PIDN:AA332755.1; GSPTB:GN00139
C:Genetics:
A:Gene: At2g04580
A:Map position: 2

Query Match 50.0%; Score 5; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPVCD 9
11111

Db 117 HPVCD 121

RESULT 15

ZWECAP
mucA protein - Escherichia coli plasmid pKM101
C:Species: Escherichia coli
C:Date: 28-Dec-1987 #sequence_revision 31-Dec-1996 #text_change 28-May-1999
C:Accession: D23157; JQ0451
R:Perry, K.L.; Elledge, S.J.; Mitchell, B.B.; Marsh, L.; Walker, G.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 4331-4335, 1985
A:Title: umuBC and mucAB operons whose products are required for UV light- and chemie
A:Reference number: A23157; MUID:85242678
A:Accession: D23157
A:Molecule type: DNA
A:Residues: 1-145 <PEP>
A:Cross-references: GB:M13388; NID:gi50798; PIDN:AAA9827.1; PID:gi50794
R:Tanooka, H.
submitted to JIPID, May 1990
A:Reference number: JQ0451
A:Contents: muc364
A:Accession: JQ0451
A:Molecule type: DNA
A:Residues: 1-12, 'R', 13-145 <TAN>
C:Comment: This is one of the two proteins encoded by the mucAB operon, the plasmid-b
operon is controlled by recA and lexA proteins.
C:Genetics:
A:Gene: mucB

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A: Genome: plasmid
 C: Superfamily: lexA repressor
 C: Keywords: induced mutagenesis; SOS mutagenesis
 Query Match 50.0%; Score 5; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EHPVC 8
 Db 139 EHPVC 143

Search completed. October 23, 2002, 12:20:50
 Job time : 19 secs

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Sequence 3, Appl
Sequence 1, Appl
Sequence 3, Appl
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Sequence 11, Appl
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Sequence 4, Appl
Sequence 7, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 31, Appl

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30 35 59.3 120 4 US-09-214-214A-1
31 35 59.3 120 4 US-09-214-214A-3
32 35 59.3 120 4 US-09-255-953-1
33 35 59.3 120 4 US-09-255-953-3
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35 35 59.3 120 5 PCT-US95-06918-1
36 35 59.3 240 3 US-08-910-691-11
37 35 59.3 257 1 US-08-451-947-4
38 35 59.3 257 2 US-08-424-826A-4
39 35 59.3 257 3 US-08-910-691-7
40 35 59.3 257 5 PCT-US91-06950-4
41 35 59.3 2035 1 US-08-046-585-5
42 34.5 58.5 2035 1 US-08-393-703-5
43 34.5 58.5 2035 5 PCT-US93-1121-5
44 34.5 58.5 2035 5 PCT-US93-1121-5
45 34 57.6 120 4 US-09-060-552-31

ALIGNMENTS

RESULT 1
US-08-420-235B-19
; Sequence 19, Application US/08420235B
; Patent No. 5801042
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF INVENTIONS: 47
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/420.235B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-420-235B-19

Query Match 67.8%; Score 40; DB 1; Length 404;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 LGHPVCD 9
DB 225 LGHPVCD 232

GenCore version 5.1.3
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OM protein - protein search, using sw model

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Title: US-09-613-355D-3
Perfect score: 59
Sequence: 1 NLGHPVCD 10

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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	40	67.8	404	4	Sequence 19, Appl
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4	37	62.7	371	2	Sequence 8, Appl
5	35	59.3	117	4	Sequence 7, Appl
6	35	59.3	117	4	Sequence 5, Appl
7	35	59.3	118	4	Sequence 3, Appl
8	35	59.3	118	4	Sequence 7, Appl
9	35	59.3	119	1	Sequence 5, Appl
10	35	59.3	119	1	Sequence 3, Appl
11	35	59.3	119	2	Sequence 2, Appl
12	35	59.3	119	3	Sequence 12, Appl
13	35	59.3	119	3	Sequence 2, Appl
14	35	59.3	119	3	Sequence 5, Appl
15	35	59.3	119	4	Sequence 5, Appl
16	35	59.3	119	4	Sequence 6, Appl
17	35	59.3	119	4	Sequence 6, Appl
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27	35	59.3	120	3	Sequence 3, Appl

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Wed Oct 23 14:06:13 2002

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RESULT 2
US-08-793-624-19
; Sequence 19, Application US/08793624C
; Patent No. 6150093
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 45185-C-PCT-US/JPW
; CURRENT APPLICATION NUMBER: US/08/793,624C
; CURRENT FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-19

Query Match 67.8%; Score 40; DB 4; Length 404;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGEHPVCD 9
DB 225 LGESPVC 232

RESULT 3
PCT-US95-10194-19
; Sequence 19, Application PC/TUS9510194
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York
; APPLICANT: City
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10194
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/NSC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-793-624-19

Query Match 67.8%; Score 40; DB 5; Length 404;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

PCT-US95-10194-19

QY 2 LGEHPVCD 9
DB 225 LGESPVC 232

RESULT 4
US-08-837-593-8
; Sequence 8, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-837-593-8

Query Match 62.7%; Score 37; DB 2; Length 371;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGEHPVCD 10
DB 330 INEEPVCDS 338

RESULT 5
US-09-214-214A-7
; Sequence 7, Application US/09214214A
; Patent No. 6211150
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenson, Susan I.

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us-09-613-355d-3_1.ra1

Wed Oct 23 14:06:13 2002

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; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/214,214A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: PCT/US97/12609
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Human
; US-09-214-214A-7

Query Match          59.3%; Score 35; DB 4; Length 117;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
Db 9 GEYSVCDS 16

RESULT 6
US-09-255-953-7
; Sequence 7, Application US/09255953
; Patent No. 6271364
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yin
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/255,953
; CURRENT FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: 08/684,353
; EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; OTHER INFORMATION: human NT-3.
; US-09-255-953-7

Query Match          59.3%; Score 35; DB 4; Length 117;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
Db 9 GEYSVCDS 16

RESULT 7
US-09-214-214A-5
; Sequence 5, Application US/09214214A
; Patent No. 6211150
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/214,214A
; US-09-214-214A-5

Query Match          59.3%; Score 35; DB 4; Length 117;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
Db 9 GEYSVCDS 16

RESULT 8
US-09-255-953-5
; Sequence 5, Application US/09255953
; Patent No. 6271364
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yin
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/255,953
; CURRENT FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: 08/684,353
; EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; OTHER INFORMATION: human NT-3.
; US-09-255-953-5

Query Match          59.3%; Score 35; DB 4; Length 118;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
Db 10 GEYSVCDS 17

RESULT 9
US-07-979-630-3
; Sequence 3, Application US/07979630
; Patent No. 5488099
; GENERAL INFORMATION:
; APPLICANT: Persson, et al.
; TITLE OF INVENTION: Multifunctional Neurotrophic Factors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; US-07-979-630-3

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/979,630
  FILING DATE: 20-NOV-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/847,369
  FILING DATE: 06-MAR-1992
NAME:
ATTORNEY/AGENT INFORMATION:
  NAME: Kempler Ph.D., Gail M.
  REGISTRATION NUMBER: 32,143
  REFERENCE/DOCKET NUMBER: REG 41
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 914-347-7000
  TELEFAX: 914-347-2113
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 119 amino acids
    TYPE: amino acid
    STRANDEDNESS: unknown
    TOPOLOGY: unknown
    MOLECULE TYPE: protein
US-07-979-630-3

Query Match          59.3%; Score 35; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 GERPYCDS 10
      ||: ||||
DB      9 GEYSVCDs 16

RESULT 10
US-08-440-049-2
: Sequence 2, Application US/08440049
: Patent No. 5728803
: GENERAL INFORMATION:
: APPLICANT: Urfer, Poman
: APPLICANT: Presta, Leonard G.
: APPLICANT: Winslow, John W.
: TITLE OF INVENTION: PANOTROPIC NEUROTROPIC FACTORS
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,049
: FILING DATE: 12-May-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/253937
: FILING DATE: 03-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Timothy E.
: REGISTRATION NUMBER: 16,700
: REFERENCE/DOCKET NUMBER: P0905C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881

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us-09-613-355d-3_1.rai

Wed Oct 23 14:06:13 2002

NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-5

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDs 10
DB 9 GEYSVCDs 16

RESULT 14
US-08-910-691-12
Sequence 12, Application US/08910691
Patent No. 6015552
GENERAL INFORMATION:
APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/074,969
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
NAME: NEJNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STPE UP
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-910-691-12

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDs 10

NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-5

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDs 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-2

Query Match 59.3%; Score 35; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDs 10
DB 9 GEYSVCDs 16

RESULT 13
US-08-970-865-5
Sequence 5, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-No. 6005081-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDs 10

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DB 9 GEYSVCDS 16
||: ||||

RESULT 15
US-08-581-662-2
: Sequence 2, Application US/08581662
: Patent No. 6121235
: GENERAL INFORMATION:
: APPLICANT: Gao, Wei-Qiang
: TITLE OF INVENTION: Treatment of Balance Impairments
: FILE REFERENCE: P0981
: CURRENT APPLICATION NUMBER: US/08/581,662
: CURRENT FILING DATE: 1995-12-29
: NUMBER OF SEQ ID NOS: 36
: SEQ ID NO 2
: LENGTH: 119
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-581-662-2

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
||: ||||
DB 9 GEYSVCDS 16

Search completed: October 23, 2002, 12:11:31
Job time : 14 secs

Wed Oct 23 14:06:10 2002

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Pusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders P.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sriden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Sriden-Kiamos I., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Tector C., Turner F., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003429; AAF45908.1;
DR FlyBase: FBgn029686; CG2941.
SQ SEQUENCE 889 AA: 102407 MW: 7D9C8718E24813EC CRC64;

Query Match 70.0%; Score 7; DB 5; Length 889;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPVC 8
DB 309 LGHPVC 315
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RESULT 2
Q9R2H0 PRELIMINARY: PRT: 414 AA.
ID Q9R2H0
AC Q9R2H0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 45.0 KDA PROTEIN.
GN DR00015.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001827; AAF12684.1;
DR TIGR: DR00015;
DR InterPro: IPR002372; Bac_PQQ_repeat.
DR Pfam: PF01011; Bacterial_PQQ_4.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 414 AA: 45017 MW: 0859847AFD10D7D5 CRC64;

Query Match 60.0%; Score 6; DB 16; Length 414;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPV 7
DB 301 LGHPV 306
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RESULT 3
Q19953 PRELIMINARY: PRT: 596 AA.
ID Q19953
AC Q19953;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 70.0 KDA PROTEIN.
GN F32A5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phabditida; Phabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998)
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pauley A.;
RT "The sequence of C. elegans cosmid F32A5.";
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20864; AAK68355.1;
DR InterPro: IPR001005; Myb_DNA_bind.
DR InterPro: IPR00822; Cnf-C2H2.
DR Pfam: PF00249; myb_DNA-binding; 1.
DR SMART: SM00395; SANT; 1.
DR PROSITE: PS0090; MYB_3; 1.
DR PROSITE: PS00328; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 596 AA: 69975 MW: 5626A6A81C0048F9 CRC64;

Query Match 60.0%; Score 6; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8
DB 19 GEHPVC 24
|||||

RESULT 4
Q78479 PRELIMINARY: PRT: 87 AA.
ID Q78479
AC Q78479;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VIRAL SAMPLE IC33, V3 REGION (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Gieselski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Taffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
RL Science 256:1165-1171(1992).

```

DR EMBL: M90962; AAA44567.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 87
FT SEQUENCE 87 AA; 9657 MW; 8104141943CD4863 CRC64;
SQ
Query Match 50.0%; Score 5; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEH 5
Db 79 NLGEH 83
RESULT 5
Q91V99 PRELIMINARY; PRT: 116 AA.
AC Q91V99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
DE REV PROTEIN.
GN REV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V11035;
RX MEDLINE=20418941; PubMed=10954895;
RA Janssens W., Salminen M.O., Laukkanen T., Reymond L.,
RA Van der Auwera G., Colebunders R., McCutchan F.E., Van der Groen G.;
RT "Near full-length genome analysis of HIV type 1 CRF02_AG subtype C and
RT CRF02_AG subtype G recombinants";
RL AIDS Res. Hum. Retroviruses 16:1183-1189(2000).
DR EMBL: AJ276595; CAB82222.1;
DR InterPro: IPR000625; REV.
DR Pfam: PF00424; REV; 1.
DR SEQUENCE 116 AA; 12900 MW; 8147CE6b1655969B CRC64;
SQ
Query Match 50.0%; Score 5; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GEHPV 7
Db 104 GEHPV 108
RESULT 6
Q9YBB8 PRELIMINARY; PRT: 116 AA.
AC Q9YBB8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 12.4 KDA PROTEIN APE1679.
GN APE1679.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1";
RL DNA Res. 6:83-101(1999).
DR EMBL: AP00062; BAA80680.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 116 AA; 12416 MW; 74008D4327518C81 CRC64;
Query Match 50.0%; Score 5; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GEHPV 7
Db 91 GEHPV 95
RESULT 7
Q9VUZ3 PRELIMINARY; PRT: 119 AA.
AC Q9VUZ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CGS157 PROTEIN.
GN CGS157.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George P.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer V.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.P., Miklos G.L.G.,
RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Peinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-f., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";

Wed Oct 23 14:06:10 2002

```

RL Science 287:2185-2195(2000)
CC - SIMILARITY: RELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF003528; AAF49529.1; -.
DR HSSP: P04166; IAWP.
DR FlyBase: FBgn0036575; CG5157.
DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 119 AA, 12622 MW, 2BACE178AS138BEF CRC64;

Query Match 50.0%; Score 5; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHP 6
DB 36 LGHP 40

RESULT 8
Q9VY32 PRELIMINARY; PRT: 124 AA.
ID Q9VY32
AC Q9VY32; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG14415 PROTEIN.
GN CG14415.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gorayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon P.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003495; AAF48373.1; -.
DR FlyBase: FBgn0030568; CG14415.
SQ SEQUENCE 124 AA, 13568 MW, E8139B765C943F57 CRC64;

Query Match 50.0%; Score 5; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHP 6
DB 22 LGHP 26

RESULT 9
Q9SI05 PRELIMINARY; PRT: 143 AA.
ID Q9SI05
AC Q9SI05; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE
GN AT2G04580.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.F., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.B., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayan L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC007231; AAD32755.1; -.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 143 AA, 15900 MW, FCEDEFC52F68FAD CRC64;

Query Match 50.0%; Score 5; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPVCD 9
DB 117 HPVCD 121

RESULT 10
Q91GY3 PRELIMINARY; PRT: 148 AA.
ID Q91GY3
AC Q91GY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MAJOR CAPSID PROTEIN (FRAGMENT).
GN L1.

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OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA60.1;
 RA Antonsson A., Hazard K., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY040279; AAK74161.1;
 FT NON_TER 1
 FT NON_TER 148
 SQ SEQUENCE 148 AA; 16489 MW; D0A8961B564670C9 CRC64;

Query Match 50.0%; Score 5; DB 12; Length 148;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10
 Db 124 PVCDS 128

RESULT 11

ID Q91GY2 PRELIMINARY; PRT; 148 AA.
 AC Q91GY2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MAJOR CAPSID PROTEIN (FRAGMENT).
 GN L1.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA60.2;
 RA Antonsson A., Hazard K., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY040280; AAK74162.1;
 FT NON_TER 1
 FT NON_TER 148
 SQ SEQUENCE 148 AA; 16517 MW; D0B977EB58A66DD4 CRC64;

Query Match 50.0%; Score 5; DB 12; Length 148;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10
 Db 124 PVCDS 128

RESULT 12

ID Q02476 PRELIMINARY; PRT; 162 AA.
 AC Q02476; Q85081;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE BETA-C PROTEIN.
 OS Poa semilantent virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.
 OX NCBI_TaxID=12328;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96204567; PubMed=8623558;
 RA Solov'yev A.G., Savenkov E.I., Agranovsky A.A., Morozov S.Y.;
 RT "Comparisons of the genomic cis-elements and coding regions in RNA

RT beta components of the hordeiviruses barley stripe mosaic virus,
 RT lychmis ringspot virus, and poa semilantent virus.";
 RL Virology 219:9-18(1996).
 RN [2]
 RP SEQUENCE OF 9-162 FROM N.A.
 RX MEDLINE=92356087; PubMed=1645144;
 RA Agranovsky A.A., Karasev A.V., Novikov V.K., Lunina N.A., Loginov S.;
 RA Tyulkina L.G.;
 RT "Poa semilantent virus, a hordeivirus having no internal polydisperse
 RT poly(A) in the 3' non-coding region of the RNA genome.";
 RL J. Gen. Virol. 73:2385-2392(1992).
 DR EMBL; M81486; AAB05579.1;
 SQ SEQUENCE 162 AA; 18195 MW; 21EE3F104778261B CRC64;

Query Match 50.0%; Score 5; DB 12; Length 162;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7
 Db 105 GEHPV 109

RESULT 13

ID Q07914 PRELIMINARY; PRT; 168 AA.
 AC Q07914;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CHROMOSOME XII PEAKING FRAME OFF YLR008C.
 GN YLR008C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vandenbol M., Portetelle D., Hilger F.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z73180; CAA97530.1;
 DR SGD; S0003995; YLR008C.
 DR InterPro; IPR001623; DnaJ_N.
 DR Pfam; PF00226; DnaJ; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00076; DnaJ_2; 1.
 SQ SEQUENCE 168 AA; 17910 MW; 9CBF71CA50A0F341 CRC64;

Query Match 50.0%; Score 5; DB 3; Length 168;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7
 Db 62 GEHPV 66

RESULT 14

ID Q916Y7 PRELIMINARY; PRT; 172 AA.
 AC Q916Y7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN PA0145.
 GN PA0145.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.

us-09-613-355d-3.rspt

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OX NCBI_TaxID=287;
RN {}
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.F.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT *Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AE004452; AAG03535.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 172 AA: 18448 MW: 47F0EF465D6C51C9 CRC64;

Query Match 50.0%; Score 5; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 122 LGEHP 126

RESULT 15
Q9K8Y6 PRELIMINARY; PRT; 179 AA.
AC Q9K8Y6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BH2866 PROTEIN.
GN BH2866.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN {}
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiram C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001516; BA065851.1; -.
DR InterPro; IPR002819; HD.
DR InterPro; IPR003607; HDC.
DR Pfam; PF01966; HD; 1.
DR SMART; SM00471; HDC; 1.
KW Complete proteome.
SQ SEQUENCE 179 AA: 20576 MW: 4182BD2CFFACAC9F CRC64;

Query Match 50.0%; Score 5; DB 16; Length 179;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 94 LGEHP 98

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Search completed. October 23, 2002, 12:20:28
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:11:34 : Search time 25 Seconds

(without alignments)
69,198 Million cell updates/sec

Title: US-09-613-355d-3

Perfect score: 59

Sequence: 1 NLGHPVCD5 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:

- 1: sp-archaea:
- 2: sp-bacteria:
- 3: sp-fungi:
- 4: sp-human:
- 5: sp-invertebrate:
- 6: sp-mammal:
- 7: sp-mmc:
- 8: sp-organelle:
- 9: sp-phage:
- 10: sp-plant:
- 11: sp-rodent:
- 12: sp-virus:
- 13: sp-vertebrate:
- 14: sp-unclassified:
- 15: sp-rvirus:
- 16: sp-bacteriaph:
- 17: sp-archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	72.9	889	5 Q9W4N9	Q9W4N9 drosophila
2	41	69.5	148	12 Q91GY3	Q91GY3 human papil
3	41	69.5	148	12 Q91GY2	Q91GY2 human papil
4	41	69.5	224	12 Q81990	Q81990 human papil
5	40	67.8	404	12 Q98141	Q98141 kaposi's sa
6	39	66.1	241	13 Q90W38	Q90W38 bothrops ja
7	39	66.1	324	13 Q9XY95	Q9XY95 lampetra fl
8	39	66.1	479	11 Q9D468	Q9D468 mus musculu
9	39	66.1	596	5 Q19953	Q19953 caenorhabdi
10	39	66.1	5170	5 Q17490	Q17490 caenorhabdi
11	39	66.1	6994	5 Q17343	Q17343 caenorhabdi
12	38	64.4	186	16 Q9JUF2	Q9JUF2 neisseria m
13	38	64.4	253	16 Q9JF26	Q9JF26 neisseria m
14	38	64.4	544	5 Q19339	Q19339 caenorhabdi
15	38	64.4	1529	3 Q9Y7C6	Q9Y7C6 aspergillus
16	37	62.7	108	13 Q98T10	Q98T10 anguilla an

17	37	62.7	116	13 Q98TH9	Q98TH9 anquilla an
18	37	62.7	371	10 Q9AYN8	Q9AYN8 nicotiana t
19	37	62.7	664	2 Q9RKL3	Q9RKL3 streptomyce
20	36	61.0	97	1 P70723	P70723 acidianus a
21	36	61.0	342	12 Q65844	Q65844 beet wester
22	36	61.0	395	2 Q69347	Q69347 vibrio sp.
23	36	61.0	454	10 Q40922	Q40922 pseudotsuga
24	36	61.0	676	10 Q4MUN5	Q4MUN5 arabidopsis
25	36	61.0	705	10 Q9SV85	Q9SV85 arabidopsis
26	36	61.0	734	10 Q9LWZ0	Q9LWZ0 arabidopsis
27	36	61.0	1037	4 Q9BX69	Q9BX69 homo sapien
28	36	61.0	1453	10 Q9AKV0	Q9AKV0 arabidopsis
29	36	61.0	1529	10 Q81068	Q81068 arabidopsis
30	35.5	60.2	359	4 Q96S99	Q96S99 homo sapien
31	35	59.3	79	13 Q9W7K1	Q9W7K1 pseudonaja
32	35	59.3	79	13 Q9W7K0	Q9W7K0 pseudonaja
33	35	59.3	129	11 Q9WU16	Q9WU16 mesocricetu
34	35	59.3	146	12 Q9WGF4	Q9WGF4 human papil
35	35	59.3	210	10 Q9PM00	Q9PM00 arabidopsis
36	35	59.3	241	6 Q9N182	Q9N182 macaca fusc
37	35	59.3	241	13 Q9DE29	Q9DE29 crocalus du
38	35	59.3	282	2 Q9S4F4	Q9S4F4 leptospira
39	35	59.3	286	13 Q91988	Q91988 xiphophorus
40	35	59.3	294	11 Q91XB4	Q91XB4 mus musculu
41	35	59.3	363	16 Q9PBW0	Q9PBW0 xylella fas
42	35	59.3	382	5 Q01933	Q01933 caenorhabdi
43	35	59.3	388	12 Q41927	Q41927 mutid helige
44	35	59.3	422	10 Q9FKH8	Q9FKH8 arabidopsis
45	35	59.3	508	16 Q9Z878	Q9Z878 chlamydia p

ALIGNMENTS

RESULT 1

Q9W4N9	Q9W4N9	PRELIMINARY:	PRT:	889 AA.
AC	Q9W4N9			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	CG2941 PROTEIN.			
GN	CG2941.			
OS	Drosophila melanogaster (fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Ananadides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George P.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Holt J.G., Nelson C.P., Miklos G.L.G.,			
RA	Abril J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Beasley E.M.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam J.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs P.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003429; AAF45908.1; -;
 DR FlyBase; FBgn0029686; CG2941.
 SQ SEQUENCE 889 AA; 102407 MW; 7D9C8718E24813EC CRC64;

Query Match 72.9%; Score 43; DB 5; Length 889;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPVC 8

Db 309 LGEHPVC 315

RESULT 2

ID Q91GY3 PRELIMINARY; PRT; 148 AA.
 AC Q91GY3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MAJOR CAPSID PROTEIN (FRAGMENT).
 GN L1.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA60.1;
 RA Antonsson A., Hazard K., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY040279; AAK74161.1; -;
 DR EMBL: AY040279; AAK74161.1; -;
 FT NON_TER 1 1
 FT NON_TER 148 148
 SQ SEQUENCE 148 AA; 16489 MW; D0A8961B564670C9 CRC64;

Query Match 69.5%; Score 41; DB 12; Length 148;
 Best Local Similarity 69.2%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGEH----PVCDS 10

Db 116 LGEHWDVAPVCDs 128

RESULT 3

ID Q91GY2 PRELIMINARY; PRT; 148 AA.
 AC Q91GY2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MAJOR CAPSID PROTEIN (FRAGMENT).
 GN L1.
 OS Human papillomavirus.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FA60.2;
 RA Antonsson A., Hazard K., Hansson B.G.;
 RT "Skin HPV found on foreheads."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY040280; AAK74162.1; -;
 DR EMBL: AY040280; AAK74162.1; -;
 FT NON_TER 1 1
 FT NON_TER 148 148
 SQ SEQUENCE 148 AA; 16517 MW; D0B977EB56A66D04 CRC64;

Query Match 69.5%; Score 41; DB 12; Length 148;
 Best Local Similarity 69.2%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGEH----PVCDS 10

Db 116 LGEHWDVAPVCDs 128

RESULT 4

ID Q81990 PRELIMINARY; PRT; 224 AA.
 AC Q81990;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CAPSID PROTEIN L1 (FRAGMENT).
 GN L1.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VS102-4;
 RC MEDLINE=94340583; Pubmed=8062252;
 RA Shamanin V., Glover M., Rausch C., Proby C., Leigh I.M., zur Hause H.,
 RA Villiers E.M.;
 RT "Specific types of HPV found in benign proliferations and carcinomas of the skin in immunosuppressed."
 RL Cancer Res. 54:4610-4613(1994).
 DR EMBL: X79946; CAA56294.1; -;
 DR InterPro; IPR002210; PV_capsid_L1.
 DR Pfam; PF00500; late_protein_L1; 1.
 DR PRINTS; PR00865; HPVcapsidL1.
 DR PRODOM; PD000544; PV_capsid_L1; 1.
 FT NON_TER 1 1
 FT NON_TER 224 224
 SQ SEQUENCE 224 AA; 24755 MW; 52D6FFF377432BEE CRC64;

Query Match 69.5%; Score 41; DB 12; Length 224;
 Best Local Similarity 69.2%; Pred. No. 4.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGEH----PVCDS 10

Db 57 LGEHWDKAPVCDs 59

RESULT 5

ID Q98141 PRELIMINARY; PRT; 404 AA.
 AC Q98141; O12570;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE ORF 23.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

us-09-613-355d-3_1.rspt

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OC Gamaherpesvirinae: Rhadinovirus.
 OX NCBI_TaxID=37296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96099469; PubMed=8523568;
 RA Moore P.S., Gao S.J., Dominguez G., Cesarman E., Lungu O.,
 RA Knowles D.M., Garber P., Pellett P.E., McGeoch D.J., Chang Y.;
 RT "Primary characterization of a herpesvirus agent associated with
 RT Kaposi's sarcoma."
 RL J. Virol. 70:549-558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97048116; PubMed=8892957;
 RA Cesarman E., Nador R.G., Bai F., Bohenzky R.A., Russo J.J.,
 RA Moore P.S., Chang Y., Knowles D.M.;
 RT "Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
 RT receptor and cyclin D homologs which are expressed in Kaposi's sarcoma
 RT and malignant lymphoma."
 RL J. Virol. 70:8218-8223(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97094384; PubMed=8939871;
 RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
 RT "Molecular mimicry of human cytokine and cytokine response pathway
 RT genes by KSHV."
 RL Science 274:1739-1744(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97121480; PubMed=8962146;
 RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
 RT (HHV8)."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX Russo J.J., Bohenzky P.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97296220; PubMed=9151804;
 RA Neipel F., Albrecht J.C., Fleckenstein B.;
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
 RT human herpesvirus 8: determinants of its pathogenicity?";
 RL J. Virol. 71:4187-4192(1997).
 DR EMBL: U75698; AAC57104.1;
 DR EMBL: U40377; AAC57104.1;
 DR EMBL: U93872; AAB08394.1;
 DR EMBL: U93872; AAB08394.1;
 SQ SEQUENCE 404 AA; 45171 MW; 88B4D2382C97FAE4 CPG64;
 Query Match 67.8%; Score 40; DB 12; Length 404;
 Best Local Similarity 87.5%; Pred. No. 12; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LGHPVCD 9
 DB 225 LGSPVCD 232
 RESULT 6
 Q90W38 PRELIMINARY; PRT: 241 AA.
 ID Q90W38
 AC Q90W38;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PUTATIVE NEUTROTROPIC GROWTH FACTOR.

NGF
 OS Bothrops jararacussu (Jararacussu).
 OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=VENOM GLAND;
 RA Kashima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
 RA Cintra A.C.O., Giglio J.R., Franca S.C.;
 RT "Molecular cloning and cDNA sequence of a nerve growth factor
 RT precursor from Bothrops jararacussu venomous gland."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007318; AAG12169.1;
 SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CPG64;
 Query Match 66.1%; Score 39; DB 13; Length 241;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NLGHPVCD 10
 DB 129 NRGEYSVCD 138
 RESULT 7
 Q9XY95 PRELIMINARY; PRT: 324 AA.
 ID Q9XY95
 AC Q9XY95;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NEUTROTROPIN.
 OS Lampetra fluviatilis (River lamprey).
 OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7748;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=LIVER;
 EX MEDLINE=99001404; PubMed=9786977;
 RA Hallbook F., Lundin L.G., Kullander K.;
 RT "Lampetra fluviatilis neurotrophin homolog, descendant of a
 RT neurotrophin ancestor, discloses the early molecular evolution of
 RT neurotrophins in the vertebrate subphylum."
 RL J. Neurosci. 18:8700-8711(1998).
 DR EMBL: AF071432; AAD22744.1;
 DR HSP: P20783; IBBK.
 DR InterPro, IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS50270; NGF; 2; 1
 FT CHAIN 141 324 NEUTROTROPIN.
 SQ SEQUENCE 324 AA; 35267 MW; 9D6B56C1978F8485 CPG64;
 Query Match 66.1%; Score 39; DB 13; Length 324;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GEHPVCD 10
 DB 177 GEYPACD 184
 RESULT 8
 Q9D468 PRELIMINARY; PRT: 479 AA.
 ID Q9D468
 AC Q9D468;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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Db 572 EHPACDS 578

RESULT 11

Q17343

ID Q17343 PRELIMINARY: PRT: 6994 AA.

AC Q17343

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE UNC-44 ANKYRINS.

GN UNC-44

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N2;

RX MEDLINE=95263663; PubMed=7744957;

RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.2., Zhang Y., V.I.,

RA Boontrakulpoontawe P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,

RA Sobery A.;

RT "An ankyrin-related gene (unc-44) is necessary for proper axonal

RT guidance in Caenorhabditis elegans.";

RL J. Cell Biol. 129:1081-1092(1995).

RN [2]

RP REVISIONS, AND SEQUENCE OF 6126-6994 FROM N.A.

RC STRAIN=N2;

RA Otsuka A.J.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U39847; AAB41827.1; -

DR EMBL: U21733; AAB38384.1; -

DR HSSP: P42773; 11HB.

DR InterPro: IPR002110; ANK.

DR InterPro: IPR000488; Death.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001360; Glyco_hydro_1.

DR InterPro: IPR000906; Z05.

DR Pfam: PF00023; ank_24.

DR Pfam: PF00531; death_1.

DR Pfam: PF00791; Z05; 1.

DR PRINTS: PR01415; ANKYRIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00248; ANK; 21.

DR SMART: SM00005; DEATH; 1.

DR SMART: SM00218; Z05; 1.

DR PROSITE: PS50088; ANK_REPEAT; 22.

DR PROSITE: PS50297; ANK_REPEAT; 1.

DR PROSITE: PS50017; DEATH_DOMAIN; 1.

DR PROSITE: PS00572; GLYCOSYL-HYDROL_F1_1; UNKNOWN_2.

KW ANK repeat; Repeat.

KW ANK repeat; Repeat.

SQ SEQUENCE 6994 AA; 775364 MW; 90CB449925D9923D CRC64;

Query Match 66.1%; Score 39; DB 5; Length 6994;

Best Local Similarity 85.7%; Pred. No. 3.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EHPACDS 10

DB 2396 EHPACDS 2402

RESULT 12

Q9JUF2

ID Q9JUF2 PRELIMINARY: PRT: 186 AA.

AC Q9JUF2

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE HYPOTHETICAL PROTEIN NMA1343.

GN NMA1343.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA Whitehead S., Spratt B.G., Barrall B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria

RT meningitidis 22491.";

RL Nature 404:502-506(2000).

DR EMBL: AL162755; CAB84591.1; -

DR InterPro: IPR002110; ANK.

DR SMART: SM00248; ANK; 1.

DR PROSITE: PS50088; ANK_REPEAT; 1.

DR PROSITE: PS50297; ANK_REPEAT; 1.

KW Hypothetical protein; Complete proteome.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 186 AA; 21087 MW; 01B85E3FF77DED73 CRC64;

Query Match 64.4%; Score 38; DB 16; Length 186;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLEHPVC 8

DB 98 NLEHPVC 105

RESULT 13

Q9JRZ6

ID Q9JRZ6 PRELIMINARY: PRT: 253 AA.

AC Q9JRZ6

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE CONSERVED HYPOTHETICAL PROTEIN / ANKYRIN-RELATED PROTEIN.

GN NMB1171 AND NMB1133.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WC58 / SEROGROUP B;

RX MEDLINE=20175755; PubMed=10710307;

RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,

RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

RA Gill J., Scarlato V., Masioni V., Pizza M., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

RT "Complete genome sequence of Neisseria meningitidis serogroup B strain

RT MC58.";

RL Science 287:1809-1815(2000).

DR EMBL: AE002465; AAF41556.1; -

DR EMBL: AE002462; AAF41521.1; -

DR TIGR: NMB1133; -

DR TIGR: NMB1171; -

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 1.

DR SMART: SM00248; ANK; 1.

DR PROSITE: PS50088; ANK_REPEAT; 1.

DR PROSITE: PS50297; ANK_REPEAT; 1.

KW Complete proteome.

SQ SEQUENCE 253 AA; 29197 MW; 989BA13327B9A44 CRC64;

Query Match 64.4%; Score 38; DB 16; Length 253;

Best Local Similarity 75.0%; Pred. No. 18;

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Query Match 64.4%; Score 38; DB 3; Length 1529;
 Best Local Similarity 60.0%; Pred. No. 1.2e-02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NLGEHPVCD 10
 DB 1104 NLQEGICDS 1113

Search completed. October 23, 2002, 12:15:39
 Job time : 29 secs

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NLGEHPVCD 8
 DB 165 NLEHPMC 172

RESULT 14
 Q19339 PRELIMINARY. PRT: 544 AA.
 AC Q19339;
 DT 01-JAN-1999 (TREMBLrel. 09, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE 4-COUMARATE-COA LIGASE 2 (EC 6.2.1.12) (4CL).
 GN F11A3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA McMurray A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + 4-COUMARATE + COA = AMP + PYROPHOSPHATE
 CC + 4-COUMAROYL-COA.
 CC -1- PATHWAY: BRANCH-POINT REACTIONS BETWEEN GENERAL PHENYLPROPANOID
 CC METABOLISM AND PATHWAYS LEADING TO VARIOUS SPECIFIC END PRODUCTS.
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; Z70751; CAA94751.1;
 DR HSP; P08659; 1LC1.
 DR WormPep; F11A3.1; CE05585.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP-BINDING; 1.
 DR Hypothetical protein; Ligase; Phenylpropanoid metabolism.
 KW SEQUENCE 544 AA; 60306 MW; 74C384771A1A7DFC CRC64;
 SQ

Query Match 64.4%; Score 38; DB 5; Length 544;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGEHPVCD 9
 DB 296 LAKHPICD 303

RESULT 15
 Q9Y7C6 PRELIMINARY. PRT: 1529 AA.
 ID Q9Y7C6;
 AC Q9Y7C6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ESTERASE.
 OS Aspergillus terreus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=33178;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC20542;
 RA Kennedy J., Auclair K., Kendrew S.G., Park C., Vederas J.C.,
 RA Hutchinson C.R.;
 RT "Accessory Proteins Modulate Polyketide Synthase Activity During
 RT Lovastatin Biosynthesis."
 RL Science 0:0-0(1999).
 DR EMBL; AF141924; AAD34550.1;
 DR InterPro; IPR001087; Lipase_GDSL.
 DR Pfam; PF00657; Lipase_GDSL; 1.
 SQ SEQUENCE 1529 AA; 170506 MW; 456FB780A6B531A3 CRC64;

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GenCore version 5.1.3
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October 23, 2002, 12:11:14 ; Search time 11 seconds
(without alignments)
35.200 Million cell updates/sec

OM protein - protein search, using sw model
Run on: October 23, 2002, 12:11:14 ; Search time 11 seconds
(without alignments)
35.200 Million cell updates/sec

Title: US-09-613-355d-3
Perfect score: 59
Sequence: 1 NLGHPVCS 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters. 105224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	86.4	116	1 NGF_NAJAT	P21377 naja atra (
2	51	86.4	116	1 NGF_NAJA	P01140 naja naja (
3	45	76.3	243	1 NGF_BUNMU	P34128 bungarus mu
4	37	62.7	371	1 NGF_TOHAC	Q40531 nicotiana t
5	36	61.0	117	1 NGF_DABRR	P30894 daboia russ
6	36	61.0	373	1 YIA6_YEAST	P40556 saccharomyc
7	36	61.0	656	1 YK79_MYCTU	Q10887 mycobacteri
8	36	61.0	898	1 TOPI_SINY3	P73810 synchocyst
9	35.5	60.2	738	1 ECT2_MOUSE	Q07139 mus musculu
10	35.5	60.2	883	1 ECT2_HUMAN	Q9h8v3 homo sapien
11	35	59.3	140	1 NT7_CYPCA	Q95150 cervus elap
12	35	59.3	154	1 NT3_CEREL	P21617 xenopus lae
13	35	59.3	231	1 NGF_XENLA	O73797 brachydanio
14	35	59.3	233	1 NT7_PPARE	P19093 cavia porce
15	35	59.3	241	1 NGF_CAVPO	P01139 mus musculu
16	35	59.3	241	1 NGF_MOUSE	P25427 rattus norv
17	35	59.3	241	1 NGF_PAT	P25433 gallus gall
18	35	59.3	257	1 NT3_CHICK	P20783 homo sapien
19	35	59.3	258	1 NT3_HUMAN	P20181 mus musculu
20	35	59.3	258	1 NT3_MOUSE	P18280 rattus norv
21	35	59.3	258	1 NT3_PAT	P25435 xenopus lae
22	35	59.3	260	1 NT3_XENLA	O53698 mycobacteri
23	35	59.3	261	1 TAM_MYCTU	P38696 saccharomyc
24	35	59.3	384	1 AP1_YEAST	Q9kst5 vibrio chol
25	35	59.3	469	1 TRPC_VIBCH	P32775 saccharomyc
26	35	59.3	704	1 GLGB_YEAST	P90211 tobamovirus
27	35	59.3	1616	1 RPO_TMOB	P51610 homo sapien
28	34.5	58.5	2035	1 HFC1_HUMAN	P51611 mesocricetu
29	34.5	58.5	2090	1 HFC1_MESAU	P07376 salmonella
30	34	57.6	146	1 MUCA_SALTY	P20675 praomys nat
31	34	57.6	241	1 NGF_PRANA	P44606 haemophilus
32	34	57.6	310	1 YOH1_HAEIN	P78753 schizosacch
33	34	57.6	556	1 ASNS_SCHPO	

34	34	57.6	708	1 RAFA_ECOLI	P16551 escherichia
35	34	57.6	808	1 GCS1_SCHPO	O14255 schizosacch
36	34	57.6	1061	1 TRC4_ECOLI	P27189 escherichia
37	34	57.6	2149	1 RRL_EVFVZ	P27316 rift valley
38	34	57.6	3707	1 PGBM_MOUSE	Q05793 mus musculu
39	33	55.9	107	1 YP94_YEAST	Q06835 saccharomyc
40	33	55.9	299	1 BE46_SCHPO	P54069 schizosacch
41	33	55.9	318	1 LPSA_BACNO	P39907 bacteroides
42	33	55.9	365	1 RF2_HAEIN	P43918 haemophilus
43	33	55.9	389	1 VMSA_HPBVI	P17397 hepatitis b
44	33	55.9	462	1 RD21_ARATH	P43297 arabidopsis
45	33	55.9	480	1 UCRL_MOUSE	Q9czl3 mus musculu

ALIGNMENTS

RESULT 1
NGF_NAJAT STANDARD; PRT; 116 AA.
AC P21377;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja atra (Chinese cobra), and
OS Naja naja kaouthia (Monocled cobra) (Naja naja siamensis).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Lepidodactylus: Squamata: Scleroglossa: Serpentes; Colubroidea:
OC Elapidae: Elapinae: Naja.
OX NCBI_TaxID=8656, 8649;
RN [1]
RP SEQUENCE.
RC SPECIES=N.n.atra; TISSUE=Venom;
RA MEDLINE=90147847; PubMed=2619756;
RX Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;
RT "Amino acid sequence of nerve growth factor purified from the venom
of the Formosan cobra Naja naja atra.";
RL Biochem. Int. 19:909-917(1989).
RN [2]
RP SEQUENCE.
RC SPECIES=N.n.kaouthia; TISSUE=Venom;
RA MEDLINE=91138755; PubMed=1995338;
RX Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT "Amino acid sequences of nerve growth factors derived from cobra
venoms.";
RL FEBS Lett. 279:38-40(1991).
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR, S13965; S13965.
DR HSP; P01139; 1BET.
DR InterPro, IPR002400; GF_CysKnot
DR InterPro, IPR002072; NGF.
DR Pfam, PF00243; NGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1; 1
DR PROSITE; PS0270; NGF_2; 1.
KW Growth factor.
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
SQ SEQUENCE 116 AA; 13064 MW, DAB35421093F3B06 GRC64;
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.01;

us-09-613-355d-3_1.rsp

Wed Oct 23 14:06:18 2002

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10
 Db 7 NLGHSVCDs 16

RESULT 2

NGF_NAJNA STANDARD: PRT; 116 AA.

AC P01140;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Nerve growth factor (NGF).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 NCBI_TaxID=35670;
 RN [1]
 RP SEQUENCE.

CC TISSUE=Venom;
 CC MEDLINE=91138755; PubMed=1995338;
 RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
 RT "Amino acid sequences of nerve growth factors derived from cobra
 RT venoms". 279:38-40(1991).
 RL FEBS Lett. 279:38-40(1991).
 RP [2]
 RP PRELIMINARY SEQUENCE.
 CC TISSUE=Venom;
 CC MEDLINE=76114772; PubMed=1247508;
 RA Hoque-Angeletti R.A., Frazier W.A., Jacobs J.W., Niall H.D.,
 RA Bradshaw R.A.;
 RT "Purification, characterization, and partial amino acid sequence of
 RT nerve growth factor from cobra venom".
 RL Biochemistry 15:26-34(1976).
 CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

DR PIR: A01401; NGNXXI.
 DR PIR: S13927; S13927.
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002400; GF_cysknot.
 DR PIR: PF00243; NGF.
 DR PIR: PF00243; NGF.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00268; NGF.
 DR PRINTS: PR00268; NGF.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 KW Growth factor.
 FT DISULFID 14 78 BY SIMILARITY.
 FT DISULFID 56 106 BY SIMILARITY.
 FT DISULFID 66 108 BY SIMILARITY.
 FT DISULFID 66 108 BY SIMILARITY.
 SQ SEQUENCE 116 AA; 13022 MW; DAB346B1093E7E06 CRC64;

Query Match 86.4%; Score 51; DB 1; Length 116;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 NLGHPVCDs 10
 Db 7 NLGHSVCDs 16

RESULT 3

NGF_BUNMU STANDARD: PRT; 243 AA.

AC P34128;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NCBI_TaxID=8616;
 RN [1]
 RP SEQUENCE FROM N.A.
 CC TISSUE=Venom;
 CC MEDLINE=93192074; PubMed=7916740;
 RX Danse J.M., Garnier J.M.;
 RA "Molecular cloning of a cDNA encoding a nerve growth factor precursor
 RT from the krait, Bungarus multicinctus".
 RL Growth Factors 8:77-86(1993).
 CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

DR EMBL: S56212; AAB25729.1; .
 DR HSSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR PIR: PF00243; NGF; 1.
 DR PRINTS: PR00258; NGF.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS0270; NGF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 125
 FT CHAIN 126 243
 FT DISULFID 139 204 BY SIMILARITY.
 FT DISULFID 182 232 BY SIMILARITY.
 FT DISULFID 192 234 BY SIMILARITY.
 SQ SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;

Query Match 76.3%; Score 45; DB 1; Length 243;
 Best Local Similarity 80.0%; Pred. No. 0.28;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10
 Db 132 NLGHSVCDs 141

RESULT 4

NTF6_TOBAC STANDARD: PRT; 371 AA.

AC Q40531;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Mitogen-activated protein kinase homolog NTF6 (EC 2.7.1.1) (P43).
 GN NTF6.
 OS Nicotiana tabacum (Common tobacco).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
PC STRAIN=CV PETIT HAVANA SRI;
RX MEDLINE=96061956; PubMed=7588752;
RA Wilson C., Angimayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco";
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC -----
DR EMBL: X83879; CAA58760.1; --
DR HSPSP; Q16539; IWP
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_pkinase
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 38 324 PROTEIN KINASE.
FT NP_BIND 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT MOD_RES 196 196 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 198 198 (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 198 198 (BY SIMILARITY).
SQ SEQUENCE 371 AA; 42741 MW; 4D97C41AC203C272 CRC64;
Query Match 62.7%; Score 37; DB 1; Length 371;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LGHEHPVCD 10
DB 330 INEEPVCDS 338
: | |||||
RESULT 5
NGF_DABRR ID NGF_DABRR STANDARD; PRT; 117 AA.
AC P30894;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF).
OS Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabolia.
OX NCBI_TaxID=31159;
RN [1]
SEQUENCE
TISSUE=Venom;
PC MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
RT the venom of Vipera russelli russelli";
KL Biochem. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR: S28161; S28161.
DR HSPSP; P01139; IBET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KW Glycoprotein; Growth factor.
FT DISULFID 12 77 BY SIMILARITY.
FT DISULFID 55 105 BY SIMILARITY.
FT DISULFID 65 107 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC...).
SQ SEQUENCE 117 AA; 13283 MW; A64559C5EC11F66 CRC64;
Query Match 61.0%; Score 36; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 NLGHEPVCDS 10
DB 5 NOGEFSVCDS 14
: | | |||||
RESULT 6
YIA6_YEAST ID YIA6_YEAST STANDARD; PRT; 373 AA.
AC P40556;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Putative mitochondrial carrier YIL006W.
GN YIL006W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
PC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Holsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC	EMBL, Z39113; CAA86245.1; -	
DR	PIR, S48451; S48451.	
DR	SIGD, S0001268; YIL006W.	
DR	InterPro, IPR001993; Mitoch_carrier.	
DR	Pfam, PF00153; mito_carr; 3.	
DR	PROSITE, PS00215; MITOCH_CARRIER; 2.	
DR	Hypothetical protein; Mitochondrion; Inner membrane; Repeat;	
DR	Transmembrane; Transpot.	
DR	TRANSMEM 81 101 POTENTIAL.	
DR	TRANSMEM 142 162 POTENTIAL.	
DR	TRANSMEM 166 186 POTENTIAL.	
DR	TRANSMEM 236 256 POTENTIAL.	
DR	SEQUENCE 373 AA; 41954 MW; 976C767C1D40E8DF CRC64;	
Query Match	61.0%; Score 36; DB 1; Length 373;	
Best Local Similarity	100.0%; Pred. No. 20;	
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 NLGEHP 6	
DB	209 NLGEHP 214	
RESULT 7		
ID	YK79_MYCTU STANDARD; PRT; 656 AA.	
AC	Q10687;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Hypothetical 69.8 kDa protein RV2079.	
DE	RV2079 OR MT2140 OR MC149.18.	
GN	Mycobacterium tuberculosis.	
OS	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
OX	NCBI_TaxID=1773;	
RN	[1]	
RP	SEQUENCE FROM N A	
RC	STRAIN=H37RV;	
RX	MEDLINE=98295987; PubMed=9634230;	
RA	Cole S.T., Brosch K., Parkhill J., Garnier T., Churcher C., Harris D.,	
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekka F.,	
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	
RA	Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,	
RA	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	
RA	Olivier S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares K.,	
RA	Sultston J.E., Taylor K., Whitehead S., Barrell B.G..	
RT	*Deciphering the biology of Mycobacterium tuberculosis from the	
RT	complete genome sequence.*	
RL	Nature 393:537-544(1998).	
CC	[2]	
CC	SEQUENCE FROM N A.	
CC	STRAIN=CDC 1551 / Oshkosh;	
CC	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,	
CC	Peterson J., Deboy K., Dodson R., Gwinn M.L., Haft D., Hickey E.,	
CC	Kollman J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,	
CC	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,	
CC	Bishai W.,	
CC	*Whole genome comparison of Mycobacterium tuberculosis clinical and	
CC	laboratory strains.*	
CC	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
CC	-!- SIMILARITY: SOME, TO M.TUBERCULOSIS RV0963C.	
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CC	or send an email to license@isb-sib.ch).	

CC	EMBL, Z73966; CAA98192.1; -	
DR	EMBL, AE007063; AAK46422.1; -	
DR	TIGR, MT2140; -	
DR	Tuberculin; RV2079; -	
KW	Hypothetical protein; Complete proteome.	
FT	CONFLICT 47 47 Y->C (IN REF. 2).	
SQ	SEQUENCE 656 AA; 69823 MW; 9DFB74A58809D3E4 CRC64;	
Query Match	61.0%; Score 36; DB 1; Length 656;	
Best Local Similarity	75.0%; Pred. No. 35;	
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	3 GEHPVCD5 10	
DB	71 GEHPINDS 78	
RESULT 8		
ID	TOP1_SYNY3 STANDARD; PRT; 898 AA.	
AC	P73810;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (relaxing enzyme)	
DE	(Untwisting enzyme) (Swivelase).	
GN	TOPIA OR SLR2058.	
OS	Synechocystis sp. (strain PCC 6803).	
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.	
OX	NCBI_TaxID=1148;	
RN	[1]	
RP	SEQUENCE FROM N A	
RX	MEDLINE=97061201; PubMed=8905231;	
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,	
RA	Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,	
RA	Hisouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,	
RA	Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,	
RA	Yanada M., Yasuda M., Tabata S.;	
RT	*Sequence analysis of the genome of the unicellular cyanobacterium	
RT	Synechocystis sp strain PCC6803. II. Sequence determination of the	
RT	entire genome and assignment of potential protein-coding regions.*	
FL	DNA Res. 3:169-136(1996).	
CC	-!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASE LEADS TO THE	
CC	CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.	
CC	-!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded	
CC	DNA, followed by passage and rejoining.	
CC	-!- SUBUNIT: MONOMER (BY SIMILARITY).	
CC	-!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA	
CC	BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN	
CC	WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS	
CC	AT ONE END OF THE ENZYME-SEVERED DNA STRAND.	
CC	-!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE	
CC	FAMILY.	
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us-09-613-355d-3_1.rsp

Wed Oct 23 14:06:18 2002

KW Guanin-nucleotide releasing factor; Repeat; Proto-oncogene.
 FT DOMAIN 1 76 BRCT 1.
 FT DOMAIN 91 179 BRCT 2.
 FT DOMAIN 277 466 DH.
 FT DOMAIN 500 619 PH.
 SQ SEQUENCE 738 AA, 83685 MW, 3D279C8F1570C681 0PF64;
 Query Match 60.2% Score 35.5; DB 1; Length 738;
 Best Local Similarity 77.8% Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 NLGEHPVCD 9
 :|||||
 Db 505 SLGEHP-CD 512

RESULT 10
 ECT2_HUMAN STANDARD; PRT: 883 AA.
 ID ECT2_HUMAN Q9NSV8;
 AC Q9NSV8; Q9NSV8; Q9NSV8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ECT2 protein (Epithelial cell transforming sequence 2 oncogene).
 GN ECT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isoda T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Naga K., Sugano S., Aotsuka S., Yoshikawa Y.,
 RA Matsunawa Y., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.,
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 631-883 FROM N.A.
 RC TISSUE=Testis;
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS HIGHLY SPECIFICALLY TO RHOA, PHOC AND RAC
 CC PROTEINS, BUT DOES NOT APPEAR TO CATALYZE GUANINE NUCLEOTIDE
 CC EXCHANGE (By similarity).
 CC -!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-146 is the
 CC Initiator.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AK023267; BAB14498.1;
 CC EMBL; AK023267; BAA91624.1;
 CC EMBL; AL137710; CAB70886.1;
 CC MIM: 600586;
 CC InterPro: IPR001357; BRCT.
 CC InterPro: IPR001331; GDS_CDC24.
 CC InterPro: IPR001849; PH.
 CC InterPro: IPR000219; RHOGEF.
 CC Pfam: PF00533; BRCT; 2.
 CC Pfam: PF00621; RHOGEF; 1.
 CC SMART: SM00292; BRCT; 2.
 CC SMART: SM00233; PH; 1.
 CC SMART: SM00325; RHOGEF; 1.
 CC PROSITE: PS50172; BRCT; 2.

DR SMART: SM00436; TOP1bc; 1.
 DR SMART: SM00493; TOP1m; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA binding; Complete proteome.
 FT ACT_SITE 320 330 DNA CRELEASE (BY SIMILARITY)
 SQ SEQUENCE 898 AA; 99340 MW; 9416665977398EB3 CRC64;
 Query Match 61.0% Score 36; DB 1; Length 898;
 Best Local Similarity 100.0% Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLGEHP 6
 :|||||
 Db 721 NLGEHP 726

RESULT 9
 ECT2_MOUSE STANDARD; PRT: 738 AA.
 ID ECT2_MOUSE Q07139;
 AC Q07139;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ECT2 protein (Epithelial cell transforming sequence 2 oncogene).
 GN ECT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 93218723; PubMed=8464478;
 RA Miki T., Smith C.L., Long J.E., Eva A., Fleming T.P.;
 RT "Oncogene ect2 is related to regulators of small GTP-binding
 RT proteins.";
 RL Nature 362:462-465(1993).
 RN [2]
 RP ERRATUM.
 RA Miki T., Smith C.L., Long J.E., Eva A., Fleming T.P.;
 RL Nature 364:737-737(1993).
 CC -!- FUNCTION: BINDS HIGHLY SPECIFICALLY TO RHOA, PHOC AND RAC
 CC PROTEINS, BUT DOES NOT APPEAR TO CATALYZE GUANINE NUCLEOTIDE
 CC EXCHANGE. TRUNCATION OF THE N-TERMINUS PUTS THE PROTEIN IN AN
 CC ACTIVATED STATE.
 CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS. ALSO DETECTABLE
 CC IN KIDNEY, LIVER AND SPLEEN.
 CC -!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
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 CC EMBL; L11316; AAA37536.1;
 CC MGD; MGI:95281; Ect2.
 CC InterPro: IPR001357; BRCT.
 CC InterPro: IPR001331; GDS_CDC24.
 CC InterPro: IPR001849; PH.
 CC InterPro: IPR000219; RHOGEF.
 CC Pfam: PF00533; BRCT; 2.
 CC Pfam: PF00621; RHOGEF; 1.
 CC SMART: SM00292; BRCT; 2.
 CC SMART: SM00233; PH; 1.
 CC SMART: SM00325; RHOGEF; 1.
 CC PROSITE: PS50172; BRCT; 2.
 CC PROSITE: PS50010; DH; 2; 1.
 CC PROSITE: PS00741; DH; 1; 1.
 CC PROSITE: PS50003; PH_DOMAIN; 1.

us-09-613-355d-3_1.rsp

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DR PROSITE: PS50010; DH_2: 1.
DR PROSITE: PS00741; DH_1: 1.
DR PROSITE: PS50003; PH_DOMAIN: FALSE_NEG.
KW Guanine-nucleotide releasing BRCT 1.
FT DOMAIN 140 229 BRCT 1.
FT DOMAIN 235 323 BRCT 2.
FT DOMAIN 421 610 DH.
FT DOMAIN 421 610 PH.
FT DOMAIN 644 763 PH.
FT CONFLICT 855 883
FT
FT
SQ SEQUENCE 883 AA, 100058 MW, 156F4DAF717364DD CRC64:

Query Match 60.2%; Score 35.5; DB 1; Length 883;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 NLGHPVCD 9
Db 649 SLGHP-CD 656

RESULT 11
NT7_CYPCA STANDARD: PRT: 140 AA.
AC 09474:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-7 precursor (NT-7) (Fragment).
GN NT7 OR NT7 OR NNT.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=9618228;
RA Lai K.-O., Fu W.-Y., Ip F.C.F., Ip N.Y.;
RT "Cloning and expression of a novel neurotrophin, NT-7, from carp.";
RL Mol. Cell. Neurosci. 11:64-76(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
CC EMBL: U94949; AAC25632.1; -.
CC HSSP: P01139; 1BTG.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF; 1.
CC PRINTS: PR00268; NGF.
CC ProDom: PD002052; NGF; 1.
CC SMART: SM00140; NGF; 1.
CC PROSITE: PS00248; NGF_1; 1.
CC PROSITE: PS50270; NGF_2; 1.
CC Growth factor.
CC NON_TER 1 1
CC PROPEP <1 7
CC CHAIN 8 140
CC DISULFID 21 101
CC DISULFID 64 129
CC DISULFID 89 131
CC VARIANT 70 70 I -> V.
CC VARIANT 95 95 E -> K.
CC SEQUENCE 140 AA; 15855 MW; 3F5E0BCE2601B0FC CRC64;

Query Match 59.3%; Score 35; DB 1; Length 140;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCD 10
Db 143 GEYSVCD 150

RESULT 13
NGF_XENLA STANDARD: PRT: 231 AA.
ID NGF_XENLA
AC P21617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

```

DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinali B., Pierandrei-Analdi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RP SEQUENCE OF 170-211 FROM N.A.
RX TISSUE=Liver.
RA MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Perisson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -!- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X55716; CAA39249.1; ALT_INIT.
DR PIR: S14481; S14481.
DR HSP: P01139; LBET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: P00268; NGF.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL 1 18
FT PROPEP 19 114
FT CHAIN 115 231
FT DISULFID 128 193
FT DISULFID 171 221
FT DISULFID 181 223
FT CARBOHYD 63 63
FT CARBOHYD 107 107
FT CARBOHYD 158 158
FT CARBOHYD 158 158
SQ SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;
Query Match 59.3%; Score 35; DB 1; Length 231;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 GEHPVCDs 10
DB 123 GEYSVCDs 130
NT7_BRARE
ID NT7_BRARE STANDARD; PRT; 233 AA.
AC 073797;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-7 precursor (NT-7) (ZNT-7).
GN NTF7 OR NT7.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98198571; PubMed=9580190;
RA Nilsson A.-S., Fainzilber M., Falck P., Ibanez C.F.;
RT "Neurotrophin-7: a novel member of the neurotrophin family from the
RT zebrafish."
RL FEBS Lett. 424:285-290(1998).
CC -!- FUNCTION: RECOMBINANT ZNT-7 WAS ABLE TO BIND TO THE HUMAN P75
CC NEUROTROPHIN RECEPTOR AND TO INDUCE TYROSINE PHOSPHORYLATION OF
CC THE RAT TRKA RECEPTOR TYROSINE KINASE, ALBEIT LESS EFFICIENTLY
CC THAN RAT NGF. ZNT-7 DID NOT INTERACT WITH RAT TRKB OR TRAC,
CC INDICATING A SIMILAR RECEPTOR SPECIFICITY AS NGF.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: AF055906; AAC41272.1; -.
DR HSP: P01139; LBET.
DR ZFIN: ZDB-GENE-990415-176; ntf7.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: P00268; NGF.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL 1 19
FT PROPEP 20 97
FT CHAIN 98 233
FT DISULFID 110 190
FT DISULFID 153 218
FT DISULFID 178 220
SQ SEQUENCE 233 AA; 26423 MW; AD0FCE96DF52C454 CRC64;
Query Match 59.3%; Score 35; DB 1; Length 233;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 GEHPVCDs 10
DB 105 GEYSVCDs 112
RESULT 15
NGF_CAVPO
ID NGF_CAVPO STANDARD; PRT; 241 AA.
AC P19093;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

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HP SEQUENCE FROM N.A.
 RC TISSUE-Prostate;
 RX MEDLINE=89177243; PubMed=2926397;
 RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
 RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
 from the guinea pig prostate gland.";
 RL J. Neurochem. 52:1203-1209(1989).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 DR PIR: JLO097; JLO097.
 DR HSP: P01139; IBET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR PRODOM: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF_1; 1.
 DR PROSITE: PS00270; NGF_2; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 121 BETA-NERVE GROWTH FACTOR.
 FT CHAIN 122 241 BY SIMILARITY.
 FT DISULFID 136 201 BY SIMILARITY.
 FT DISULFID 179 229 BY SIMILARITY.
 FT DISULFID 189 231 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 241 AA, 26821 MW, 2F4E26E197804RF4 CPC64;

Query Match 59.3%; Score 35; DB 1; Length 241;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLGEHPVCD5 10
 DB 129 HMGEFSVCDS 138

Search completed, October 23, 2002, 12:15:05
 Job time : 13 secs

Oct 23 14:06:17 2002

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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:13:29 : Search time 16 seconds
(without alignments)
60.056 Million cell updates/sec

Title: US-09-613-355D-3
Perfect score: 59
Sequence: 1 NLGHPVCDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues 283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.71.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	86.4	116	1 NGNJXI	nerve growth facto
2	51	86.4	116	2 A58566	nerve growth facto
3	51	86.4	246	2 A59218	nerve growth facto
4	45	76.3	224	2 I51193	nerve growth facto
5	41	69.5	224	2 S48779	L1 protein - human
6	39	66.1	925	2 T16235	hypothetical prote
7	39	66.1	5170	2 T15348	hypothetical prote
8	38	64.4	186	2 C81903	hypothetical prote
9	38	64.4	253	2 D81118	conserved hypothet
10	38	64.4	544	2 T20741	hypothetical prote
11	37	62.7	116	2 JC7620	guanylin precursor
12	37	62.7	371	2 S51320	mitogen-activated
13	37	62.7	1317	2 B41950	retrovirus-related
14	36	61.0	117	2 S28161	nerve growth facto
15	36	61.0	373	2 S48451	probable membrane
16	36	61.0	454	2 JC4848	cysteine proteinas
17	36	61.0	656	2 B70766	hypothetical prote
18	36	61.0	676	2 F85107	hypothetical prote
19	36	61.0	705	2 T04052	DNA topoisomerase
20	36	61.0	898	2 S74903	RNA-directed DNA p
21	36	61.0	1529	2 T02730	WD-40 repeat prote
22	36	61.0	1747	2 AC1842	hypothetical prote
23	35.5	60.2	297	2 T46414	transforming prote
24	35.5	60.2	738	2 S32372	nerve growth facto
25	35	59.3	235	2 S14481	beta-nerve growth
26	35	59.3	241	2 JL0097	neurotrophin-3 pre
27	35	59.3	245	2 I56370	neurotrophin-3 pre
28	35	59.3	257	2 C40304	neurotrophin-3 pre
29	35	59.3	257	2 I50400	neurotrophin-3 pre

neurotrophin-3 pre
hypothetical prote
hippocampus-derive
neurotrophin-6 - s
nerve growth facto
DNA primase XF2025
conserved hypothet
hypothetical prote
centractin ACN3 -
indore-3-glycerol
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
1.4-alpha-glucan b
hypothetical prote

ALIGNMENTS

RESULT 1

NGNJXI

C:Species: Naja naja naja (Indian cobra)

C>Date: 30-Nov-1980 #sequence_revision 25-Apr-1997 #text_change 17 Mar-2000

C:Accession: S13927; A01401

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venom.

A:Reference number: S13927; MUID:91138755

A:Accession: S13927

A:Molecule type: protein

A:Residues: 1-116<INO>

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we

R:Hoque-Angelletti, R.A.; Frazier, W.A.; Jacobs, J.W.; Niall, H.D.; Bradshaw, R.A.

Biochemistry 15, 26-34, 1976

A:Title: Purification, characterization, and partial amino acid sequence of nerve gro

A:Reference number: A01401; MUID:76114772

A:Accession: A01401

A:Molecule type: protein

A:Residues: 1-11, P', L3', 14', B', 16', 'TBT', 20-21, 'GV', 23-27, 'N', 29-31, 'AS', 34, 'S', 36-48,

15-116<HOG>

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we

C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 86.4%; Score 51; DB 1; Length 116;

Best Local Similarity 90.0%; Pred. No. 0 035; 1; Indels 0; Gaps 9;

Matches 9, Conservative 0; Mismatches 1; Indels 0; Gaps 9;

Qy 1 NLGHPVCDS 10

Db 7 NLGHSVCDS 16

RESULT 2

A58566

C:Species: Naja naja atra (Chinese cobra)

C>Date: 16-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997

C:Accession: A58566

P:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.

Biochem. Int. 19, 909-917, 1989

A:Title: Amino acid sequence of nerve growth factor purified from the venom of the

A:Reference number: A58566; MUID:90147847

A:Accession: A58566

A:Molecule type: protein

us-09-613-355d-3_1.rpr

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```

A:Residues: 1-116 <QDA>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 NLGHPVCDs 10
    | | | | |
Db  7 NLGHSVCDs 16

RESULT 3
A59218
nerve growth factor beta chain precursor - monocled cobra
C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: A59218; S13965
R:Seiby, M.J.; Edwards, R.H.; Rutter, W.J.
J. Neurosci. Res. 18, 293-298, 1987
A:Title: Cobra nerve growth factor: structure and evolutionary comparison.
A:Reference number: A59218; MUID:88090976
A:Accession: A59218
A:Molecule type: mRNA
A:Residues: 1-246 <SEL>
R:Inoue, S.; Oda, T.; Kovama, J.; Ikeda, K.; Hayashi, K.
FEBS Lett. 279, 38-40, 1991
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
A:Reference number: S13927; MUID:91138755
A:Accession: S13965
A:Molecule type: protein
A:Residues: 131-246 <INO>
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:1-23/Domain: signal sequence #status predicted <SIG>
F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>
F:144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 246;
Best Local Similarity 90.0%; Pred. No. 0.075;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 NLGHPVCDs 10
    | | | | |
Db 137 NLGHSVCDs 146

RESULT 4
I51193
nerve growth factor precursor - many-banded krait
C:Species: Bungarus multicinctus (many-banded krait)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51193
R:Danse, J.M.; Garnier, J.M.
Growth Factors 8, 77-86, 1993
A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the
A:Reference number: I51193; MUID:93192074
A:Accession: I51193
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-243 <DAN>
A:Cross-references: GB:S5612, NID:q566298, PDB:AA25729, 1: PID:q566299
C:Superfamily: nerve growth factor beta chain

Query Match      76.3%; Score 45; DB 2; Length 243;

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Best Local Similarity 80.0%; Pred. No. 0.94;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 NLGHPVCDs 10
    | | | | |
Db 132 NLGHSVCDs 141

RESULT 5
S48779
L1 protein - human papillomavirus (isolate vs102-4) (fragment)
N:Alternate names: capsid protein L1
C:Species: human papillomavirus
A:Variety: isolate vs102-4
C:Date: 10-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
R:Shamanin, V.; Glover, M.; Rausch, C.; Proby, C.; Leigh, I.M.; zur Hause, H.; Villie
submitted to the EMBL Data Library, June 1994
A:Description: Specific types of HPV found in benign proliferations and carcinomas of
A:Reference number: S48779
A:Accession: S48779
A:Molecule type: DNA
A:Residues: 1-224 <SHA>
A:Cross-references: EMBL:X79946; NID:q562410; PDB:CAA56234, 1: PID:q562311
A:Experimental source: isolate vs102-4
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match      69.5%; Score 41; DB 2; Length 224;
Best Local Similarity 69.2%; Pred. No. 4.7;
Matches      9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY  2 LGEH----PVCDS 10
    | | | | |
Db  57 LGEHWDKAPVCDs 69

RESULT 6
T16235
hypothetical protein F32A5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16235
R:Pauley, A.
submitted to the EMBL Data Library, July 1995
A:Description: the sequence of C. elegans cosmid F32A5.
A:Reference number: Z18482
A:Accession: T16235
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-925 <PAU>
A:Cross-references: EMBL:U40864; NID:q669026; PDB:q669027; PDB:AA46660, 1: GESP:F32A
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F32A5.1
A:Introns: 36/3; 142/1, 172/2, 263/3; 349/1, 521/1, 535/1, 572/2, 812/1

Query Match      66.1%; Score 39; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 45;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 GEHPVC 8
    | | | | |
Db  6 GEHPVC 11

RESULT 7
T15348
hypothetical protein B0350.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15348
R:Gattung, S.

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submitted to the EMBL Data Library, February 1996
 A:Description: The sequence of *C. elegans* cosmid B0350.
 A:Reference number: Z18332
 A:Accession: T15348
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5170 <GAT>
 A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208877; PIDN:AAA93447.1; CESP:B0350
 C:Genetics:
 A:Gene: CESP:B0350.1
 A:Introns: 48/1: 5039/3; 5116/3

Query Match 66.1%; Score 39; DB 2; Length 5170;
 Best Local Similarity 85.7%; Pred. No. 2: 6e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EHPVCDs 10
 DB 572 EHPACDS 578

RESULT 8
 C81903
 hypothetical protein NMA1343 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup
 C:Species: *Neisseria meningitidis*
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 S.; Holtroyd, S.; Jagsels, K.; Leather, S.; Moulle, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A:Reference number: AB1775; MUID:20222556
 A:Accession: C81903
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <PAR>
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84591.1; PID:g738001
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1343

Query Match 64.4%; Score 38; DB 2; Length 186;
 Best Local Similarity 75.0%; Pred. No. 14; Indels 1; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 NLGHPVPC 8
 DB 98 NLEHPMC 105

RESULT 9
 DB1118
 conserved hypothetical protein / ankyrin-related protein NMB1133, NMB1171 [imported] - *N*
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: DB1118; AB1114
 R:Telletlin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: AB1000; MUID:20175755
 A:Accession: DB1118
 A:Molecule type: DNA
 A:Residues: 1-253 <TET>
 A:Cross-references: GB:AE002098; NID:g7226363; PIDN:AAF41521.1; PID:g722637
 A:Experimental source: serogroup B, strain MC58
 A:Accession: AB1114
 A:Molecule type: DNA
 A:Residues: 1-253 <TET>
 A:Cross-references: GB:AE002465; GB:AE002098; NID:g7226401; PIDN:AAF41556.1; PID:g722640
 A:Experimental source: serogroup B, strain MC58

C:Genetics:
 A:Gene: NMB1133; NMB1171

Query Match 64.4%; Score 38; DB 2; Length 253;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVPC 8
 DB 165 NLEHPMC 172

RESULT 10
 T20741
 hypothetical protein FliA3.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
 C:Accession: T20741
 R:McMurry, A.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z19318
 A:Accession: T20741
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-544 <WIL>
 A:Cross-references: EMBL:Z70751; PIDN:CAA94751.1; GSPDB:GN00023; CESP:FliA3.1
 A:Experimental source: clone FliA3
 C:Genetics:
 A:Gene: CESP:FliA3.1
 A:Map position: 5
 A:Introns: 70/3, 108/1, 217/2; 282/3; 375/4; 505/1
 C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 F:67-536/Domain: acetate-CoA ligase homology; <ACL>

Query Match 64.4%; Score 38; DB 2; Length 544;
 Best Local Similarity 62.5%; Pred. No. 41; Indels 1; Gaps 0;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGHPVPC 9
 DB 296 LAKHPICD 303

RESULT 11
 JC7620
 guanylin precursor, long form - European eel
 C:Species: *Anguilla anguilla* (European eel)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7620
 R:Comrie, M.M.; Cutler, C.P.; Gramb, G.
 Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
 A:Title: Cloning and expression of guanylin from the European eel (*Anguilla anguilla*)
 A:Reference number: JC7620; MUID:21139737; PMID:11243845
 A:Accession: JC7620
 A:Molecule type: mRNA
 A:Residues: 1-116 <COM>
 A:Cross-references: GB:AJ301673
 C:Comment: This protein, a member of a family of heat-stable peptides, is a potent ex
 axis. This peptide signalling system plays a role in osmoregulation in euryhaline te
 C:Superfamily: guanylin
 C:Keywords: heat-stable protein; osmoregulation
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-116/Product: guanylin precursor, long form #status predicted <MAT>
 F:33-39/Region: homologous #status predicted
 F:69-114/Region: highly conserved #status predicted

Query Match 62.7%; Score 37; DB 2; Length 116;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
 DB 62 NLGSHAVCSN 71

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C:Superfamily: nerve growth factor beta chain

Query Match 61.0%; Score 36; DB 2; Length 117;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGHPVCD 10
 Db 5 NOGFSVCD 14

RESULT 15

S48451

Probable membrane protein YIL006w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 31-Mar-2000

C:Accession: S48451

R:Rowley, N.

submitted to the EMBL Data Library, August 1994

A:Reference number: S48442

A:Accession: S48451

A:Molecule type: DNA

A:Residues: 1-373 <ROW>

A:Cross-references: GB:247047, EMBL:238113, NID:3623937, FID:3763340, MIPS:YIL006w

C:Genetics:

A:Map position: 9L

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat hemology

C:Keywords: duplication; mitochondrion; transmembrane protein

F:74-167/Domain: ADP,ATP carrier protein repeat hemology <ACP1>

F:79-95/Domain: transmembrane #status predicted <TM1>

F:173-264/Domain: ADP,ATP carrier protein repeat hemology <ACP2>

F:236-252/Domain: transmembrane #status predicted <TM2>

F:275-365/Domain: ADP,ATP carrier protein repeat hemology <ACP3>

Query Match 61.0%; Score 36; DB 2; Length 373;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6
 Db 209 NLGHP 214

Search completed: October 23, 2002, 12:16:00
 Job time : 18 secs

RESULT 12

S51320

Mitogen-activated protein kinase 6 (EC 2.7.1.1) - common tobacco

N:Alternate names: serine/threonine-specific protein kinase p43Ntf6

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999

C:Accession: S68189, S51320

R:Wilson, C.; Anglimayer, R.; Vicente, O.; Heberle-Bors, E.

Eur. J. Biochem. 233, 249-257, 1995

A:Title: Molecular cloning, functional expression in Escherichia coli, and characterization

A:Reference number: S68189; MUID:96061956

A:Accession: S68189

A:Molecule type: mRNA

A:Residues: 1-371 <W12>

A:Cross-references: EMBL:X83879, NID:3634067, FID:3634068

C:Genetics:

A:Gene: ntf6

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:35-324/Domain: protein kinase homology <KIN>

F:44-52/Region: protein kinase ATP-binding motif

Query Match 62.7%; Score 37; DB 2; Length 371;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGHPVCD 10
 Db 330 INEHPVCD 338

RESULT 13

B41950

retrovirus-related hypothetical protein 2 - Trypanosoma cruzi retrotransposon

C:Species: Trypanosoma cruzi

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Jan-1999

C:Accession: B41950

R:Villanueva, M.S.; Williams, S.P.; Beard, C.B.; Richards, F.F.; Aksoy, S.

Mol. Cell. Biol. 11, 6139-6148, 1991

A:Title: A new member of a family of site-specific retrotransposons is present in the sp

A:Reference number: A41950; MUID:92049344

A:Accession: B41950

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1317 <VIL>

A:Cross-references: GB:M62862, NID:3162247, FID:3162249

A:Note: sequence extracted from NCBI backbone (NCBI:66378, NCBIP:66380)

Query Match 62.7%; Score 37; DB 2; Length 1317;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCD 9
 Db 30 GGPICD 36

RESULT 14

S28161

nerve growth factor beta chain - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S28161

R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochim. Biophys. Acta 1160, 287-292, 1992

A:Title: Purification and amino acid sequence of a nerve growth factor from the venom of

A:Reference number: S28161; MUID:93120151

A:Accession: S28161

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-117 <KOY>

us-09-613-355d-3_1.rag

Wed Oct 23 14:06:12 2002

Arabisopsis thalia
Arabisopsis thalia
Novel human diago
Novel human diago
Human polypeptide
Propionibacterium
Human polypeptide
Human CARD-6 prote
Human polypeptide
Human protein sequ
Novel signal trans
Novel human neopla
Human protein sequ
Human G protein as
Mutant huNT-3 1-11
Human NT-3(1-117)R
Chimeric neurotrop
NGF, mouse, Mus m
Mutant met-huNT-3
Human r-metHuNT-3
NT-3, mouse, Mus
Neurotrophin-3, R
Human neurotrophin
Mutant huNT-3 1-11
Neurotrophin-3 will
Human neurotrophin
Human NT-3(1-115)R
Nerve growth facto
NT-3 amino acid se
Chimeric neurotrop
Chimeric neurotrop
Chimeric neurotrop

12 36 61.0 118 21 AAG11707
13 36 61.0 130 21 AAG11706
14 36 61.0 180 22 ABG08318
15 36 61.0 213 22 ABG14503
16 36 61.0 222 22 AAO11203
17 36 61.0 326 22 AAU41494
18 36 61.0 596 22 AAG64029
19 36 61.0 1037 22 AAB20087
20 35.5 60.2 108 22 AAC04935
21 35.5 60.2 359 22 AAB93279
22 35.5 60.2 386 22 AAU17446
23 35.5 60.2 386 22 AAU21629
24 35.5 60.2 798 22 AAB94519
25 35.5 60.2 914 22 AAB82972
26 35 59.3 117 19 AAW52303
27 35 59.3 117 19 AAE05872
28 35 59.3 118 13 AAR21874
29 35 59.3 118 13 AAR29493
30 35 59.3 118 19 AAW52301
31 35 59.3 118 22 AAE05870
32 35 59.3 119 13 AAR29495
33 35 59.3 119 15 AAR54086
34 35 59.3 119 19 AAW48889
35 35 59.3 119 19 AAW52302
36 35 59.3 119 20 AAW81118
37 35 59.3 119 21 AAY92008
38 35 59.3 119 22 AAE05871
39 35 59.3 119 22 AAG64595
40 35 59.3 119 22 AAE05871
41 35 59.3 120 13 AAR21866
42 35 59.3 120 13 AAR21867
43 35 59.3 120 13 AAR21868
44 35 59.3 120 13 AAR21869
45 35 59.3 120 13 AAR21869

ALIGNMENTS

RESULT 1
AAM89511
ID AAM89511 standard; Protein; 73 AA.
AC AAM89511;
DT 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen SEQ ID NO:17104.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotaxtic; gene therapy; vaccine; metastasis.
XX Homo sapiens.
OS
PN WO200157182-A2.
XX
PD 09-AUG-2001
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
FR 04-FEB-2000; 2000US-0180628.
FR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216980.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	43	72.9	73	AAM89511	Human immune/haema
2	43	72.9	889	22 AAB66958	Homo sapiens
3	41	69.5	224	16 AAR98274	Papilloma virus ma
4	40	67.8	404	17 AAR97833	Kaposi's sarcoma a
5	40	67.8	404	17 AAR97833	Kaposi's sarcoma a
6	39	66.1	60	22 AAM87222	Human immune/haema
7	39	66.1	74	22 AAM87222	Human immune/haema
8	38	64.4	79	22 AAO48620	Propionibacterium
9	38	64.4	87	22 AAO48620	Propionibacterium
10	38	64.4	105	22 AAO48620	Propionibacterium
11	38	64.4	1529	21 AAY96744	A. terreus ORF1 es

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OM protein - protein search, using sw model

Run on: October 23, 2002, 12 10 29 : Search time 31 Seconds

(without alignments)
35,830 Million cell updates/sec

Title: US-09-613-355d-3

Perfect score: 59

Sequence: 1 NLGHPVCD 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1985.DAT.*
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9: /SIDSI/gcdata/geneseq/geneseq-emb1/AA1988.DAT.*
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21: /SIDSI/gcdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcdata/geneseq/geneseq-emb1/AA2001.DAT.*

wo 01/5-7-182

changed
Pub-8-9-07

CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 XX

SQ Sequence 73 AA;

Query Match 72.9%; Score 43; DB 22; Length 73;
 Best Local Similarity 75.0%; Pred. No. 3.3;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPVCD 9
 DB 40 LGQHPLCD 47

RESULT 2

ID ABB66958 standard; Protein: 889 AA.

AC ABB66958;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 27666.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-141537P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI: 2001-656860/75.

XX N-PSDB: ABL11061.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -

XX Disclosure; SEQ ID NO 27666; 21pp + Sequence Listing: English.

XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins
 XX (ABB57737-ABB72072).

XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 889 AA;

Query Match 72.9%; Score 43; DB 22; Length 889;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPVCD 8
 DB 309 LGEHPVCD 315

RESULT 3

ID AAR88274 standard; Peptide: 224 AA.

XX AAR88274;

XX 12-JUN-1996 (first entry)

XX Papilloma virus major capsid protein.

XX HP-virus 15; papilloma virus; major;

XX capsid protein; plasmid VS92.1; DSM 9140; diagnosis;

XX skin carcinomas; therapy; vaccination.

XX Papilloma virus.

XX DE4415743-A1.

XX 09-NOV-1995.

XX 04-MAY-1994; 94DE-4415743.

XX 04-MAY-1994; 94DE-4415743.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX de Villiers zur Hausen E, Leigh I, Shamanin V, zur Hausen H;
 XX WPI: 1995-383680/50.

XX N-PSDB: AAT03506.

XX DNA encoding peptide(s) of papilloma virus major capsid protein -
 XX useful for detecting papilloma virus in skin carcinoma

XX Claim 7; Fig 8; 15pp; German.

XX AAT03506 is 82.8% homologous to HP-Virus 15, encodes AAR88274 a
 XX peptide of papilloma virus (PV) major capsid protein and is
 XX expressed by the plasmid VS92-1 (DSM 9140). The DNA is useful
 XX in diagnosis, esp. to detect PV in skin carcinomas. Major capsid
 XX proteins encoded by a PV genome contg. the DNA are useful for
 XX therapy and/or vaccination.

XX Sequence 224 AA;

Query Match 69.5%; Score 41; DB 16; Length 224;

Best Local Similarity 69.2%; Pred. No. 23;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGEH----PVCD 10

DB 57 LGEHWDKAPVCD 69

RESULT 4

ID AAR97833 standard; Protein: 404 AA.

XX AAR97833;

XX 11-SEP-1996 (first entry)

XX Kaposi's sarcoma associated herpesvirus ORF23 product.

XX Kaposi's sarcoma, gamma-2 herpesvirus; KSHV; therapy; diagnosis;

XX vaccine; diagnosis; AIDS.

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XX OS Kaposi's sarcoma associated herpesvirus.
XX PN WO9615779-A1.
XX PD 30-MAY-1996.
XX PF 21-NOV-1995; 95WO-US15138.
XX PR 11-APR-1995; 95US-0420235.
XX PR 21-NOV-1994; 94US-0343101.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Chang Y, Moore PS;
XX PI WPI, 1996:268320/27.
XX DR N-PSDB; AAT30685.
XX PT Herpes virus associated with Kaposi's sarcoma - also definitive DNA
XX PT sequences, useful for diagnosis of and to develop prods. for
XX PT treatment of Kaposi's sarcoma
XX PS Claim 17; Page 203-205; 277pp; English.
XX PS Lambda clone KS5 (AAT30681) is a fragment of a newly identified human
XX CC gamma-2 herpesvirus associated with Kaposi's sarcoma (KS). KS5 has
XX CC 17 open reading frames (AAT30682-98), 15 of which are complete,
XX CC including ORF23 (AAT30685). The protein products (AAR97830-46,
XX CC respectively) of the 17 ORFs can be expressed in eukaryotic or
XX CC bacterial host cells for use as vaccines, for KS diagnosis, or for
XX CC raising antibodies.
XX SQ Sequence 404 AA;
XX SQ Query Match 67.8%; Score 40; DB 17; Length 404;
XX SQ Best Local Similarity 87.5%; Pred. No. 61;
XX SQ Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGHPVCD 9
DB 225 LGSPVCD 232

RESULT 5
AAR93609
ID AAR93609 standard; Protein: 404 AA.
XX AC AAR93609;
XX DT 13-AUG-1996 (first entry)
XX DE Kaposi's sarcoma associated herpesvirus ORF23 product.
XX KW Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis;
XX KW therapy.
XX OS Kaposi's sarcoma associated herpesvirus.
XX PN WO9606159-A1.
XX PD 29-FEB-1996.
XX PF 11-AUG-1995; 95WO-US10194.
XX PR 11-APR-1995; 95US-0420235.
XX PR 18-AUG-1994; 94US-0292365.
XX PR 21-NOV-1994; 94US-0343100.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK
XX PA (GRAN/) GRANT D E.
XX PA (VIEL/) VIELE L.
XX

PI Chang Y, Moore PS, Grant DE, Viele L;
XX DR WPI: 1996-151362/15.
XX DR N-PSDB; AAT16815.
XX PT Herpes-virus DNA associated with Kaposi's sarcoma - also associated
XX PT vectors and proteins, used in detection and vaccination.
XX XX Claim 17; Page 216-218; 305pp; English.
XX XX Kaposi's sarcoma associated herpes virus (KSHV) clone KS5 (AAT16806),
XX CC obt'd. from a KS lesion genomic library, includes 15 complete ORFs and
XX CC 2 incomplete ORFs (AAT16807-23) named according to their herpesvirus
XX CC salmuri positional homologues. The ORF23 (AAT16815) product is
XX CC given in AAR93609. KSHV proteins and peptides may be obt'd. by
XX CC incorporating encoding sequences into a vector and expression in
XX CC host cells. They are useful in vaccines or for raising antibodies of
XX CC diagnostic or therapeutic value.
XX SQ Sequence 404 AA;
XX SQ Query Match 67.8%; Score 40; DB 17; Length 404;
XX SQ Best Local Similarity 87.5%; Pred. No. 61;
XX SQ Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGHPVCD 9
DB 225 LGSPVCD 232

RESULT 6
AAM87222
ID AAM87222 standard; Protein: 60 AA.
XX AC AAM87222;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen SEQ ID NO:14815.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis.
XX XX Homo sapiens.
XX CS WO200157182-A2.
XX PN 09-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US01354.
XX PF 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 26-JUL-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.

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PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 23-AUG-2000; 2000US-0228924.
 PR 30-AUG-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229288.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231141.
 PR 08-SEP-2000; 2000US-0231144.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240460.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.

PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WFL, 2001:4834-6/52.
 N-PSDB: AAK60003.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides.
 useful for preventing, diagnosing and/or treating cancers and
 metastasis.

Claim 11: SEQ ID NO 14815; 3071pp + Sequence Listing: English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome
 that affect the activity of (I) by expressing inactive proteins or to
 supplement the patient's own production of (I). Additionally, (I)
 polynucleotides may be used to produce the secreted (I), by inserting
 the nucleic acids into a host cell and culturing the cell to express the
 protein. (I) proteins and polynucleotides may be used to prevent,
 diagnose and treat immune/hematopoietic-related diseases, especially
 cancers and cancer metastases of haematopoietic antigen genomic
 to AAK87694 represent human immune/hematopoietic antigen genomic
 sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 represent sequences used in the exemplification of the present invention.

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SQ Sequence 74 AA:
 Query Match 66.1%; Score 39, DB 22; Length 74;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GEHPVC 8
 DB 28 GEHPVC 33
 RESULT 8
 AAU60325
 ID AAU60325 standard; Protein: 79 AA.
 XX
 AC AAU60325;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #21221.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB; AAS59609.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1: SEQ ID No 21520; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 AA:
 Query Match 66.1%; Score 39, DB 22; Length 60;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GEHPVCD 10
 DB 4 GEHPVCP 11
 RESULT 7
 AAU48620
 ID AAU48620 standard; Protein: 74 AA.
 XX
 AC AAU48620;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #9516.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB; AAS59543.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1: SEQ ID No 9815; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

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Db 54 NLASHPICN 62

RESULT 11
ID AAY96744 standard; Protein: 1529 AA.

XX AC AAY96744;
XX DT 09-OCT-2000 (first entry)
XX DE A. terreus ORF1 esterase-like protein.
XX KW Lovastatin; D4B segment; monacolin J; esterase-like; ORF1; anti-lipemic;
XX KW HMG-CoA reductase inhibitor; anti-hypercholesterolaemic; anti-fungal.
XX OS Aspergillus terreus.
XX WO200037629-A2.
XX 29-JUN-2000.
XX PF 13-DEC-1999; 99WO-US29583.
XX PR 18-DEC-1998; 98US-0215694.
XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX PI Hutchinson RC, Kennedy J, Park C;
XX WPI: 2000-442660/38.
XX DR N-PSDB; AAA51296.
XX PT Increasing lovastatin or monacolin J production in an organism, for use
XX PT as antihypercholesterolemic or antifungal agents, comprises
XX PT transforming the organism with a D4B segment
XX PS Disclosure; Page 55-59; 116pp; English.

The proteins shown in AAY96744-60 are encoded by 17 genes from a
cluster in *Aspergillus terreus* (ATCC 20542), which flank the NPKS
(nonaketide polyketide synthase) gene, which is known to be required for
lovastatin production. The NPKS gene is contained within the context of
the entire gene cluster but is not indicated here (see US744350). The
genes and proteins are named "ORF" or "Lov", where "Lov" signifies genes
shown to be essential for lovastatin production. The portion of the gene
cluster between ORF1 and the mid-region of Lovf is referred to as the
"D4B segment". Increasing lovastatin, or monacolin J, production in a
lovastatin-producing organism, comprises transforming the organism with
a D4B segment, and expressing it (claimed). Lovastatin will also be
produced in non-lovastatin producing organisms (e.g. *A. nidulans*) by
transformation with the D4B segment and the entire Lovf gene. The
methods are used to increase biosynthetic production of lovastatin (with
an at least 5-fold increase) which is an anti-hypercholesterolaemic
agent, and also has some anti-fungal activity. Lovastatin inhibits the
conversion of hydroxymethylglutarylcoenzyme A (HMG-CoA) into mevalonate
by HMG-CoA reductase. The methods can also be used to increase production
of monacolin J (claimed), which has anti-fungal activity.

XX SQ Sequence 1529 AA;

Query Match 64.4%; Score 38; DB 21; Length 1529;
Best Local Similarity 60.0%; Pred. No. 5;le+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLGHPVCDS 10
|||:||||

Db 1104 NLGEGICDS 1113

RESULT 12
AAG11707
ID AAG11707 standard; Protein: 118 AA.

XX AC AAG11707;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 10527.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 04-MAY-1999; 99US-0132407.
XX 05-MAY-1999; 99US-0132484.
XX 06-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
XX 11-MAY-1999; 99US-0132863.
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XX DE
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Wed Oct 23 14:06:12 2002

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XX (HYSE-) HYSEQ INC.
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XX Drmanac RT, Liu C, Tang YT:
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XX WPI: 2001-639362/73.
DR
XX N-PSDB: AAS72505.
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XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
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XX Claim 20; SEQ ID No 38677; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
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KW food supplement; medical imaging; diagnostic; genetic disorder.
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XX (HYSE-) HYSEQ INC.
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XX Drmanac RT, Liu C, Tang YT:
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XX WPI: 2001-639362/73.
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XX N-PSDB: AAS72505.
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XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 38677; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
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 XX WPI: 2001-639362/73.
 PI N-PSDB; AAS78690.
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 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
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GenCore version 5.1.3
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10:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1989.DAT.*		10:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1989.DAT.*	
11:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1990.DAT.*		11:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1990.DAT.*	
12:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1991.DAT.*		12:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1991.DAT.*	
13:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1992.DAT.*		13:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1992.DAT.*	
14:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1993.DAT.*		14:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1993.DAT.*	
15:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1994.DAT.*		15:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1994.DAT.*	
16:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1995.DAT.*		16:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1995.DAT.*	
17:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1996.DAT.*		17:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1996.DAT.*	
18:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1997.DAT.*		18:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1997.DAT.*	
19:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1998.DAT.*		19:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1998.DAT.*	
20:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1999.DAT.*		20:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA1999.DAT.*	
21:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA2000.DAT.*		21:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA2000.DAT.*	
22:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA2001.DAT.*		22:	/SIDSL/gcgdata/	geneseq/geneseq-emb1/AA2001.DAT.*	

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	70.0	889	22	AB666958
2	6	60.0	63	22	AAU56224
3	6	60.0	63	22	AAU68556
4	6	60.0	74	22	AAU48620
5	6	60.0	180	22	ABC08318
6	6	60.0	452	22	AAU62691
7	5	50.0	31	22	AAU47444
8	5	50.0	34	17	AAU14312
9	5	50.0	34	17	AAU14314
10	5	50.0	34	17	AAU99982
11	5	50.0	35	16	AAU74411

12	5	50.0	35	16	AAU74396	Parathyroid hormon
13	5	50.0	54	22	AAU63726	Propionibacterium
14	5	50.0	58	21	AAU14258	Arabidopsis thalia
15	5	50.0	65	22	AAU50065	Propionibacterium
16	5	50.0	65	22	AAU50116	Human brain T calc
17	5	50.0	67	21	AAU14408	Rat cortactin-Bp1
18	5	50.0	75	20	AAU37877	Amino acid sequenc
19	5	50.0	76	21	AAU14257	Arabidopsis thalia
20	5	50.0	82	22	AAU49625	Propionibacterium
21	5	50.0	88	22	AAU49877	Propionibacterium
22	5	50.0	92	21	AAU02958	Human secreted pro
23	5	50.0	93	20	AAU12774	Human 5' EST secre
24	5	50.0	99	22	AAU4606	Human immune/haema
25	5	50.0	108	22	AAU04995	Human polypeptide
26	5	50.0	114	22	AAU68963	Adenovirus 5 E4orf
27	5	50.0	119	22	ABU61303	Drosophila melanog
28	5	50.0	124	22	ABU69338	Drosophila melanog
29	5	50.0	157	22	AAU19454	Human diagnostic a
30	5	50.0	174	22	AAU68878	Human RECAP polype
31	5	50.0	198	22	AAU02175	Mycobacterium xeno
32	5	50.0	199	22	AAU02180	Mycobacterium xeno
33	5	50.0	199	22	AAU02181	Mycobacterium xeno
34	5	50.0	199	22	AAU02182	Mycobacterium xeno
35	5	50.0	211	22	AAU10182	Human bone marrow
36	5	50.0	213	22	ABU14503	Novel human diagno
37	5	50.0	217	16	AAU68556	Klebsiella sp. nit
38	5	50.0	220	21	AAU35347	Arabidopsis thalia
39	5	50.0	221	21	AAU26579	Arabidopsis thalia
40	5	50.0	224	16	AAU88274	Papilloma virus ma
41	5	50.0	230	21	AAU25346	Arabidopsis thalia
42	5	50.0	239	21	AAU26578	Arabidopsis thalia
43	5	50.0	245	22	ABU03529	Novel human diagno
44	5	50.0	259	22	AAU10202	Human bone marrow
45	5	50.0	268	22	AAU48176	Thermus thermophil

ALIGNMENTS

RESULT 1	
ABU66958	ABU66958 standard; Protein; 889 AA.
ID	ABU66958 standard; Protein; 889 AA.
AC	ABU66958;
XX	
XX	26-MAR-2002 (first entry)
DT	
XX	Drosophila melanogaster polypeptide SEQ ID NO 27666.
DE	
XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
XX	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
XX	23-MAR-2000; 2000US-191637P.
PR	11-JUL-2000; 2000US-0614150.
PE	(PEKE) PE CORP NY.
XX	
PA	Venter JC, Adams M, Li PWD, Myers EW;
XX	
PI	
XX	WPI; 2001-656860/75.
DR	N-PSDB; ABU11061.
XX	
XX	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions

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CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 XX
 SQ Sequence 63 AA;
 Query Match 60.0%; Score 6, DB 22; Length 63;
 Best Local Similarity 100.0%; Fred. No. 3 2;
 Matches 6, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPV 7
 Db 41 LGHPV 46
 |||||

RESULT 3
 AAU66556
 ID AAU66556 standard; Protein; 63 AA.
 XX
 AC AAU66556;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #27452.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS59741.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 27751; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC *P. acnes* is also involved in infections of bone, joints and the central

XX
 PS
 XX Disclosure; SEQ ID NO 27666; 21pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL15175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 XX
 SQ Sequence 889 AA;
 Query Match 70.0%; Score 7, DB 22; Length 889;
 Best Local Similarity 100.0%; Fred. No. 3 2;
 Matches 7, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPVC 8
 Db 309 LGHPVC 315
 |||||

RESULT 2
 AAU56224
 ID AAU56224 standard; Protein; 63 AA.
 XX
 AC AAU56224;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #17120.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS59741.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 17419; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC *P. acnes* is also involved in infections of bone, joints and the central

nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 60.0%; Score 6; DB 22; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.2; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 2 LGEHPV 7
DB 41 LGEHPV 46
IIIIII

RESULT 4
AAU48620
ID AAU48620 standard; Protein: 74 AA.
XX AC AAU48620;
XX DT 27-FEB-2002 (first entry)
XX DE Propionibacterium acnes immunogenic protein #9516.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN W0200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-NS12865.
XX PR 21-APR-2000; 2000US-14047P
XX PR 02-JUN-2000; 2000US-208841P.
XX PR 07-JUL-2000; 2000US-216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI: 2001-616774/71.
XX N-PSDB; AAS59543.
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris -
XX Example 1: SEQ ID No 9815; 1069pp; English.
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central

nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 60.0%; Score 6; DB 22; Length 74;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8
DB 28 GEHPVC 33
IIIIII

RESULT 5
ABG08318
ID ABG08318 standard; Protein: 180 AA.
XX AC ABG08318;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #8309.
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN W0200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX N-PSDB; AAS72505.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID No 38677; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as

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presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 60.0%; Score 6; DB 22; Length 180;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6
 Db 30 NLGHP 35

RESULT 6
 AAU62691
 ID AAU62691 standard; Protein; 452 AA.

XX AAU62691;

XX 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #23587.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59628.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

XX vaccinating against and diagnosing infections, especially useful for

XX treating acne vulgaris -

XX Example 1; SEQ ID No 23886; 1069pp; English.

XX Sequences AAU30105-AAU68017 represent Propionibacterium acnes immunogenic
 XX polypeptides. The proteins and their associated DNA sequences are used in
 XX the treatment, prevention and diagnosis of medical conditions caused by
 XX *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
 XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 XX *P. acnes* is also involved in infections of bone, joints and the central
 XX nervous system, however it is particularly involved in the inflammatory
 XX lesions associated with acne vulgaris. A method for detecting the

presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

QY 2 LGHPV 7
 Db 348 LGHPV 353

RESULT 7

AAAB47444

ID AAAB47444 standard; peptide; 31 AA.

XX AAAB47444;

XX 31-OCT-2001 (first entry)

XX Entire 3rd loop from strain nH1-1715MEE (Group 2a type).

XX surface exposed loop; major outer membrane protein P5; MOMP P5;

XX non-typeable *H. influenzae*; nH1; LBI(f) peptide; B cell epitope;

XX otitis media; sinusitis; conjunctivitis;

XX lower respiratory tract infection.

XX Haemophilus influenzae.

XX WO200161013-A1.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO-EP01556.

XX 15-FEB-2000; 2000GB-0003502.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Berthet FJ, Denoel P, Poolman J, Thonnard J;

XX WPI, 2001-522599/57

XX Recombinant bacterial outer membrane protein where one or more

XX surface-exposed loops are modified is useful as a vaccine to prevent or

XX treat Haemophilus influenzae infection or associated disease, e.g.,

XX otitis media and conjunctivitis -

XX Claim 2; Page 26; 29pp; English.

XX The sequences given in AAB47439-46 represent peptides which may be used
 XX to replace one or more surface exposed loops of major outer membrane
 XX protein P5 (MOMP P5) of non-typeable *H. influenzae* (nH1). Each of
 XX these peptides contain an LBI(f) peptide which is a 19 amino acid
 XX peptide derived from the sequence of MOMP P5 from strain nH1128.
 XX representing amino acids Arg117 to Gly135. This peptide represents the
 XX third exposed loop of P5 and is a potential B cell epitope. The loops
 XX of the invention are modified in terms of being in a non-native
 XX environment in the recombinant outer membrane protein. The modified
 XX MOMP P5 may be used to induce an immune response in a mammal to
 XX prevent or treat Haemophilus influenzae infection or associated

Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 10 NLGEH 14

RESULT 9
AAW14314
ID AAW14314 standard; peptide; 34 AA.
XX AC AAW14314;
XX DT 30-APR-1997 (first entry)
XX DE Cyclic parathyroid hormone (1-34) peptide 7.
XX KW cyclic parathyroid hormone fragment; calcium-regulating activity;
XX KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
XX KW improved half life; calcium retention; bone.
XX OS Synthetic.

Key Location/Qualifiers
Modified-site 13 /note= "forms lactam bridge with Lys at position 17"
Modified-site 17 /note= "forms lactam bridge with Glu at position 13"
DE19508672-A1.
12-SEP-1996.
10-MAR-1995; 95DE-1008672.
10-MAR-1995; 95DE-1008672.
(BOEF) BOEHRINGER MANNHEIM GMBH.
Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
WPI; 1996-413519/42.

Cyclic parathyroid hormone fragments with lactam bridge - have good
in vivo half life and are useful for treating osteoporosis and
preventing epidermal cell proliferation
Claim 6; Page 13; 14pp; German.
New cyclic parathyroid hormone fragments (CPTH) have the amino acid
sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids
at the N-terminus, and are cyclised between positions 13 and 17. One of
these positions is occupied by L- or D- Orn or Lys, and the other by L-
or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
treating osteoporosis and inhibit proliferation of epidermal cells (for
treating psoriasis). The CPTH have an improved half life in vivo than
known PTH fragments, increased mitogenicity and DNA-synthesising
capacity, reduced catabolic, calcium-mobilising activity and increased
activity for calcium retention and incorporation into bone. AAW14308-16
are claimed CPTH of the invention.

Query Match 50.0%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 10 NLGEH 14

CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
respiratory tract infection.

XX Sequence 31 AA;
Query Match 50.0%; Score 5; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 21 NLGEH 25

RESULT 8
AAW14312
ID AAW14312 standard; peptide; 34 AA.
XX AC AAW14312;
XX DT 30-APR-1997 (first entry)
XX DE Cyclic parathyroid hormone (1-34) peptide 5.
XX KW cyclic parathyroid hormone fragment; calcium-regulating activity;
XX KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
XX KW improved half life; calcium retention; bone.
XX OS Synthetic.

Key Location/Qualifiers
Modified-site 13 /note= "forms lactam bridge with Orn at position 17"
Modified-site 17 /label= Orn
/note= "forms lactam bridge with Glu at position 13"
DE19508672-A1.
12-SEP-1996.
10-MAR-1995; 95DE-1008672.
10-MAR-1995; 95DE-1008672.
(BOEF) BOEHRINGER MANNHEIM GMBH.
Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
WPI; 1996-413519/42.

Cyclic parathyroid hormone fragments with lactam bridge - have good
in vivo half life and are useful for treating osteoporosis and
preventing epidermal cell proliferation
Claim 6; Page 12; 14pp; German.
New cyclic parathyroid hormone fragments (CPTH) have the amino acid
sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids
at the N-terminus, and are cyclised between positions 13 and 17. One of
these positions is occupied by L- or D- Orn or Lys, and the other by L-
or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
treating osteoporosis and inhibit proliferation of epidermal cells (for
treating psoriasis). The CPTH have an improved half life in vivo than
known PTH fragments, increased mitogenicity and DNA-synthesising
capacity, reduced catabolic, calcium-mobilising activity and increased
activity for calcium retention and incorporation into bone. AAW14308-16
are claimed CPTH of the invention.

Query Match 50.0%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 10 NLGEH 14

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metabolic bone disease; human; veterinary medicine;
iontophoretic transdermal transport; recombinant E.coli.

RESULT 10
AAR99982
ID AAR99982 standard; peptide: 34 AA.

XX AAR99982;
XX AC
XX DT 30-APR-1997 (first entry)

XX Canine parathyroid hormone peptide fragment (1-34).

XX cyclic parathyroid hormone fragment; calcium-regulating activity;
XX osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
XX improved half life; calcium retention; bone.

XX Synthetic.

XX DE19508672-AL.

XX 12-SEP-1996.

XX 10-MAR-1995; 95DE-1008672.

XX 10-MAR-1995; 95DE-1008672.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;

XX WPI: 1996-413519/42.

XX Cyclic parathyroid hormone fragments with lactam bridge - have good
XX in vivo half life and are useful for treating osteoporosis and
XX preventing epidermal cell proliferation

XX Disclosure: Page 10; 14pp; German.

XX New cyclic parathyroid hormone fragments (CPTH) have the amino acid
XX sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
XX acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
XX the N-terminus, and are cyclised between positions 13 and 17. One of
XX these positions is occupied by L- or D- Orn or Lys, and the other by L-
XX or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
XX treating osteoporosis and inhibit proliferation of epidermal cells (for
XX known psoriasis). The CPTH have an improved half life in vivo than
XX treating osteoporosis). The CPTH have an improved half life in vivo than
XX known CPTH fragments, increased mitogenicity and DNA-synthesising
XX capacity, reduced catabolic, calcium-mobilising activity and increased
XX activity for calcium retention and incorporation into bone. The
XX present sequence is that of canine PTH peptide fragment (1-34).

XX Sequence 34 AA;

Query Match 50.0%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 10 NLGEH 14

RESULT 11
AAR74411
ID AAR74411 standard; peptide: 35 AA.

XX AAR74411;

XX 01-DEC-1995 (first entry)

XX Parathyroid hormone peptide analogue, Gly12,16,28,33.

XX Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
XX osteoporosis; hypercalcaemia; hyperparathyroidism;

XX Key Location/Qualifiers

XX Modified-site 35

XX /label= "H, OTHER

XX /note= "Homoserine (Hse), Hse lactone, Hse amide or
XX residues 35-84 of PTH"

XX W09511988-A.

XX 04-MAY-1995.

XX 25-OCT-1994, 94WO-US12205.

XX 25-OCT-1993; 93US-0142551.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Oldenburg KR, Selick HE;

XX WPI: 1995-178680/23.

XX New active analogues of parathyroid hormone - with increased
XX activity, stability in serum etc., esp. for treating
XX osteoporosis, also related DNA and vectors

XX Claim 3; Page 86; 109pp; English.

XX The sequences given in AAR74411-26 represent analogues of the 34 amino
XX acid sequence of truncated human parathyroid hormone (PTH). These
XX analogues have increased activity and longer serum half life than
XX native PTH due to eg. substitution of Met residues with Leu residues and
XX replacing the carboxy Phe with Tyr. The carboxy terminal may also be
XX modified by the addition of a homoserine residue or analogue, or by the
XX addition of residues 35-84 of wild type PTH (see AAR74410). These PTH
XX analogues may be used in the treatment of osteoporosis or
XX hypercalcaemia, hyperparathyroidism or other metabolic bone diseases in
XX human or veterinary medicine. These peptides may also have increased
XX iontophoretic transdermal transport compared to wild type PTH and
XX can be produced in high yield in recombinant E.coli.

XX Sequence 35 AA;

Query Match 50.0%; Score 5; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 10 NLGEH 14

RESULT 12
AAR74396
ID AAR74396 standard; peptide: 35 AA.

XX AAR74396;

XX 30-NOV-1995 (first entry)

XX Parathyroid hormone peptide analogue, Glu13.

XX Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
XX osteoporosis; hypercalcaemia; hyperparathyroidism;
XX metabolic bone disease; human; veterinary medicine;
XX iontophoretic transdermal transport; recombinant E.coli.

XX Synthetic.

XX Key Location/Qualifiers

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PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS59634.
 XX
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 24921; 1069pp; English.
 CC
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 54 AA;
 Query Match 50.0%; Score 5; DB 22; Length 54;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 HPVCD 9
 Db 4 HPVCD 8
 RESULT 14
 AAG14258
 ID AAG14258 standard; Protein: 58 AA.
 XX
 AC AAG14258;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 14050.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PF 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR

FT Modified-site 35
 FT /label="H. OTHER
 FT /note="Homoserine (Hse), Hse lactone, Hse amide or
 FT residues 35-84 of PTH"
 PN WO9511988-A.
 XX
 PD 04-MAY-1995.
 XX
 XX 25-OCT-1994; 94WO-US12205.
 XX
 XX 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 XX Oldenburg KR, Selick HE;
 DR WPI: 1995-178880/23.
 XX
 XX New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Claim 2; Page 85; 109pp; English.
 CC
 CC The sequences given in AAR74394-409 represent analogues of the 34 amino
 CC acid sequence of truncated human parathyroid hormone (PTH). These
 CC analogues have increased activity and longer serum half life than
 CC native PTH due to substitution of Met residues with Leu residues and
 CC replacing the carboxy Phe with Tyr. The carboxy terminal may also be
 CC modified by the addition of a homoserine residue or analogue, or by the
 CC addition of residues 35-84 of wild type PTH (see AAR74410). These PTH
 CC analogues may be used in the treatment of osteoporosis or
 CC hypercalcaemia, hyperparathyroidism or other metabolic bone diseases in
 CC human or veterinary medicine. These peptides may also have increased
 CC iontophoretic transdermal transport compared to wild type PTH and
 CC can be produced in high yield in recombinant E.coli.
 XX
 SQ Sequence 35 AA;
 Query Match 50.0%; Score 5; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLGEH 5
 Db 10 NLGEH 14
 RESULT 13
 AAU63726
 ID AAU63726 standard; Protein: 54 AA.
 XX
 AC AAU63726;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #24622.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 XX 21-APR-2000; 2000US-199047P.
 PR

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PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 23-APR-1999; 990S-0130891.
PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 04-MAY-1999; 990S-0132407.
PR 05-MAY-1999; 990S-0132484.
PR 06-MAY-1999; 990S-0132486.
PR 07-MAY-1999; 990S-0132487.
PR 11-MAY-1999; 990S-013256.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 25-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 10-JUN-1999; 990S-0138847.
PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.
PR 16-JUN-1999; 990S-0139453.
PR 17-JUN-1999; 990S-0139453.
PR 18-JUN-1999; 990S-0139454.
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PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
PR 22-JUN-1999; 990S-0139899.
PR 23-JUN-1999; 990S-0140353.
PR 23-JUN-1999; 990S-0140354.
PR 24-JUN-1999; 990S-0140695.
PR 28-JUN-1999; 990S-0140823.
PR 29-JUN-1999; 990S-0140991.
PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.
PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142393.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
PR 13-JUL-1999; 990S-0143542.
PR 14-JUL-1999; 990S-0143624.
PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144325.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 19-JUL-1999; 990S-0144352.
PR 20-JUL-1999; 990S-0144632.
PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
PR 21-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145085.
PR 22-JUL-1999; 990S-0145087.
PR 22-JUL-1999; 990S-0145089.
PR 22-JUL-1999; 990S-0145192.
PR 23-JUL-1999; 990S-0145145.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.
PR 28-JUL-1999; 990S-0145951.
PR 28-JUL-1999; 990S-0146386.
PR 02-AUG-1999; 990S-0146388.
PR 02-AUG-1999; 990S-0146389.
PR 02-AUG-1999; 990S-0147038.
PR 03-AUG-1999; 990S-0147038.
PR 04-AUG-1999; 990S-0147204.
PR 04-AUG-1999; 990S-0147302.
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PR 05-AUG-1999; 990S-0147260.
PR 06-AUG-1999; 990S-0147303.
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PR 09-AUG-1999; 990S-0147493.
PR 09-AUG-1999; 990S-0147935.
PR 10-AUG-1999; 990S-0148171.
PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149175.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 25-AUG-1999; 990S-0150566.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 27-AUG-1999; 990S-0151080.
PR 31-AUG-1999; 990S-0151438.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
PR 20-SEP-1999; 990S-0154779.
PR 22-SEP-1999; 990S-0155139.
PR 23-SEP-1999; 990S-0155486.
PR 24-SEP-1999; 990S-0155689.
PR 28-SEP-1999; 990S-0156458.
PR 29-SEP-1999; 990S-0156596.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.

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XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59546.
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX Example 1: SEQ ID No 11260; 1069pp; English.
 PS
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and the central
 CC P. acnes is also involved in infections of bone, joints and the inflammatory
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 65 AA:
 Query Match 50.0%; Score 5; DB 22; Length 65;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7
 DB 3 GEHPV 7
 Search completed: October 23, 2002, 12:19:35
 Job time : 32 secs

XX 99US-0157865.
 DR 99US-0158029.
 XX 99US-0158232.
 PT 99US-0158369.
 PT 99US-0159293.
 PT 99US-0159294.
 PT 99US-0159295.
 PT 99US-0159329.
 PT 99US-0159330.
 PT 99US-0159331.
 PT 99US-0159637.
 PT 99US-0159638.
 PT 99US-0159584.
 PT 99US-0160741.
 PT 99US-0160767.
 PT 99US-0160768.
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 PT 99US-0160989.
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 PT 99US-0161406.
 PT 99US-0161359.
 PT 99US-0161360.
 PT 99US-0161361.
 PT 99US-0161920.
 PT 99US-0161992.
 PT 99US-0161993.
 PT 99US-0162142.
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 Query Match 50.0%; Score 5; DB 21; Length 58;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
 DB 2 LGEHP 6

RESULT 15
 AAU50065
 ID AAU50065 standard; Protein: 65 AA.
 XX AC AAU50065;
 XX 27-FEB-2002 (first entry)
 XX Propionibacterium acnes immunogenic protein #10961.
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX Propionibacterium acnes.
 XX WO200181581-A2.
 XX 01-NOV-2001.
 XX 20-APR-2001; 2001WO-US12865.
 XX 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX (CORI-) CORIXA CORP.
 PA Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;